

FIGURE 1

FIG. 1A

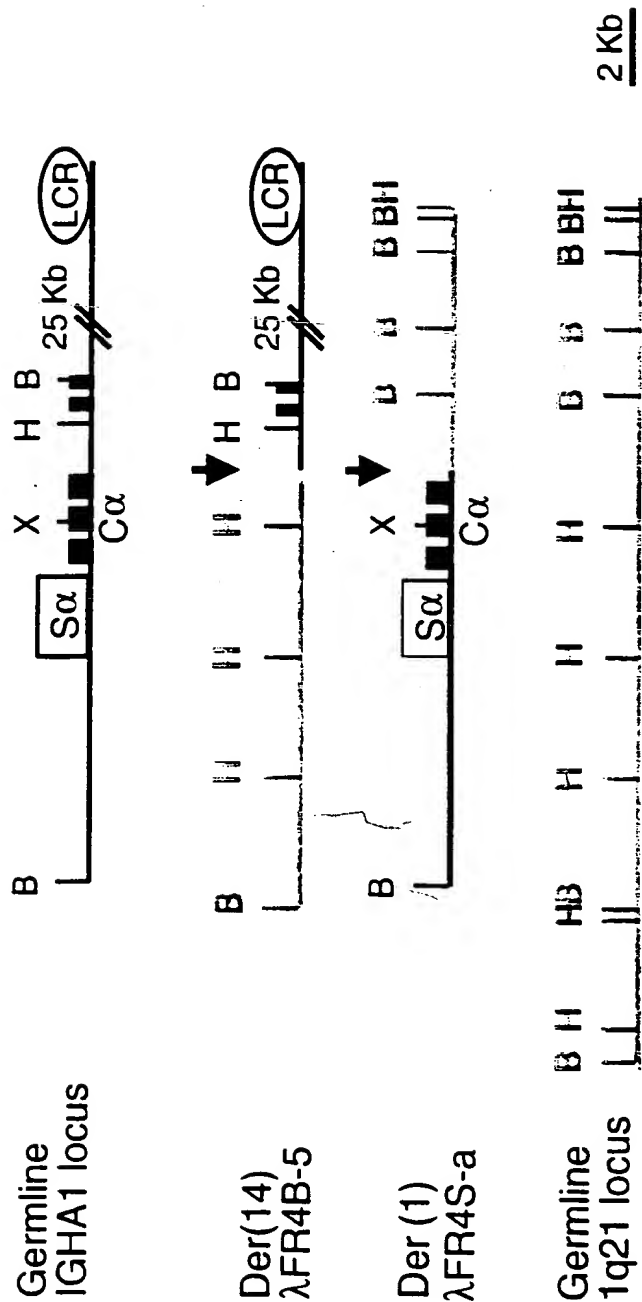


FIG. 1B

Chr 1 GGGCCTGACAGCAACITTTCTTCTACTAGTTTCATCTTAACCTTATCCTGGTAAC'TGGCGAGACAACCTGTCTTAAGTAACTGAAGGAAA  
 |||||  
 der14 GGGCCTGACAGCAACITTTCTTCTTCTACTAGTTTCATCTTAACCTTATCCTGGTAACCTGTCTTAAGTAACTGAAGGAAA  
 |||||  
 Chr 14 TCCCACTGACGCATGCAGGAAGGGGCACCTCCCTTAACCTGTCTTGTACGGGGCACAGGTGGGCACACTCACA

**FIGURE 2A**

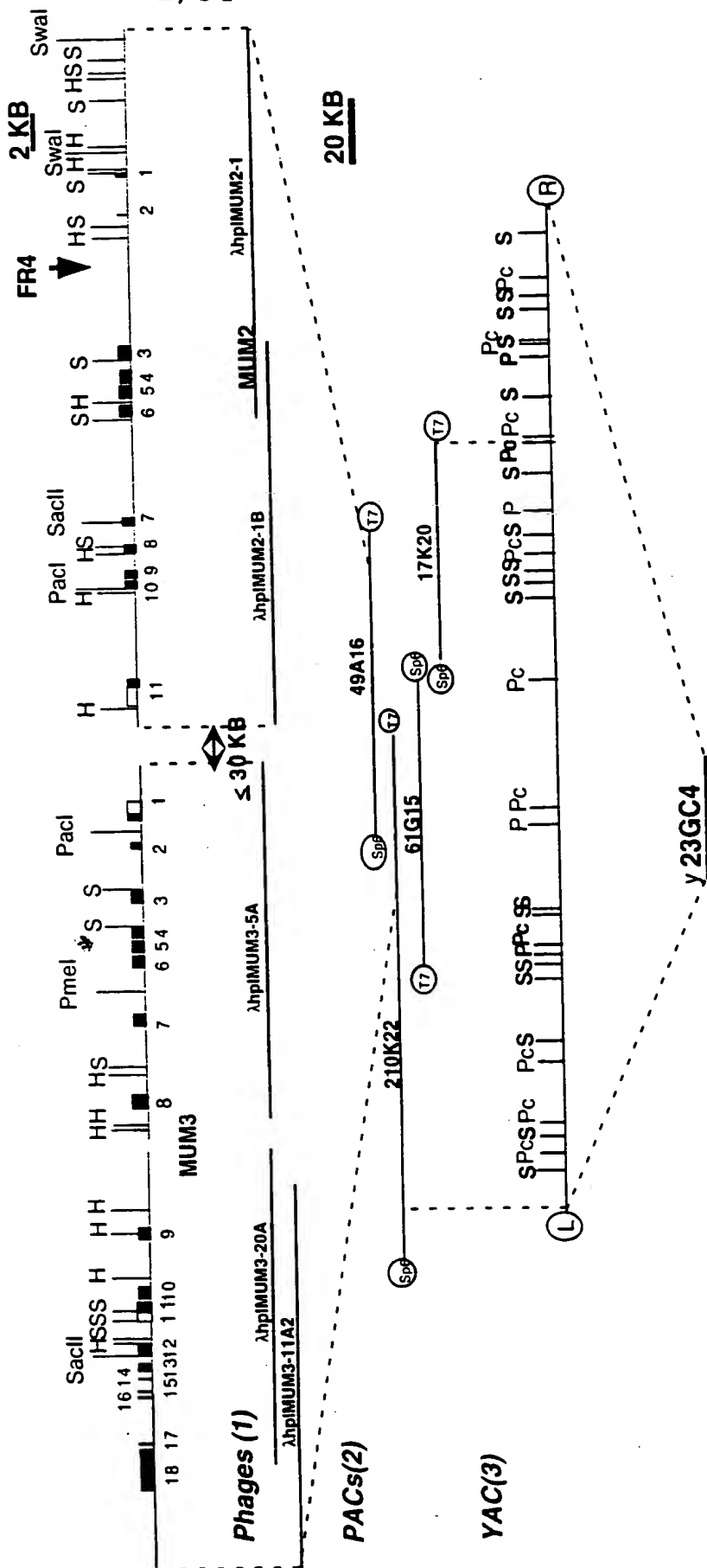


FIGURE 2B

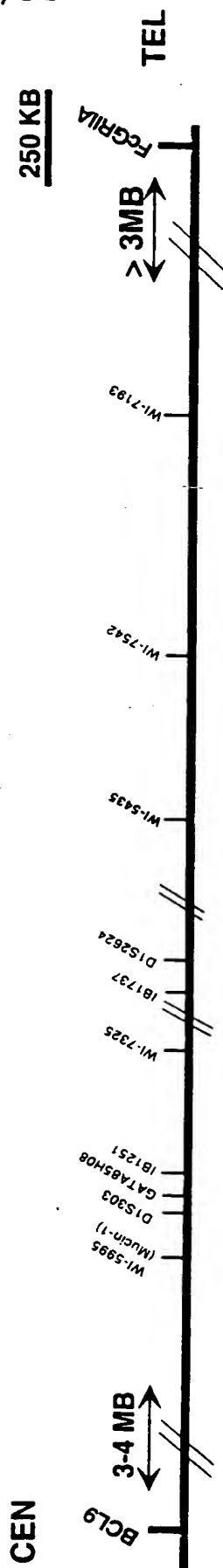


FIGURE 3

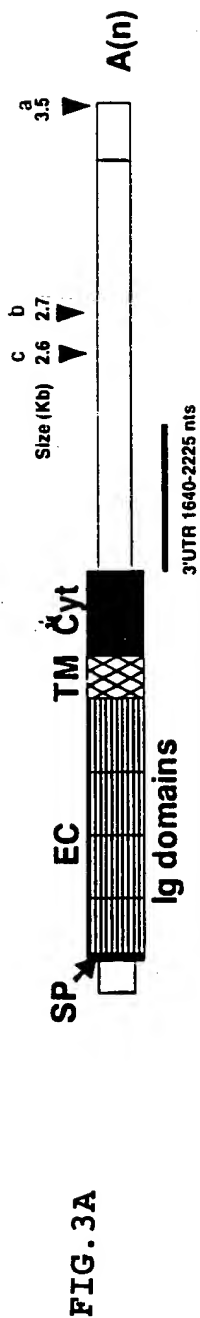


FIG. 3B

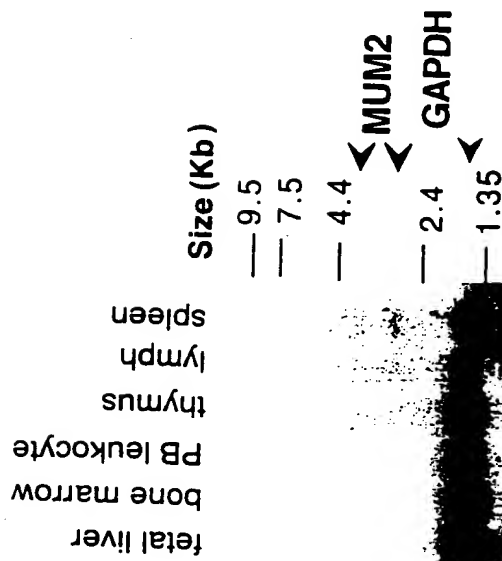


FIG. 3C

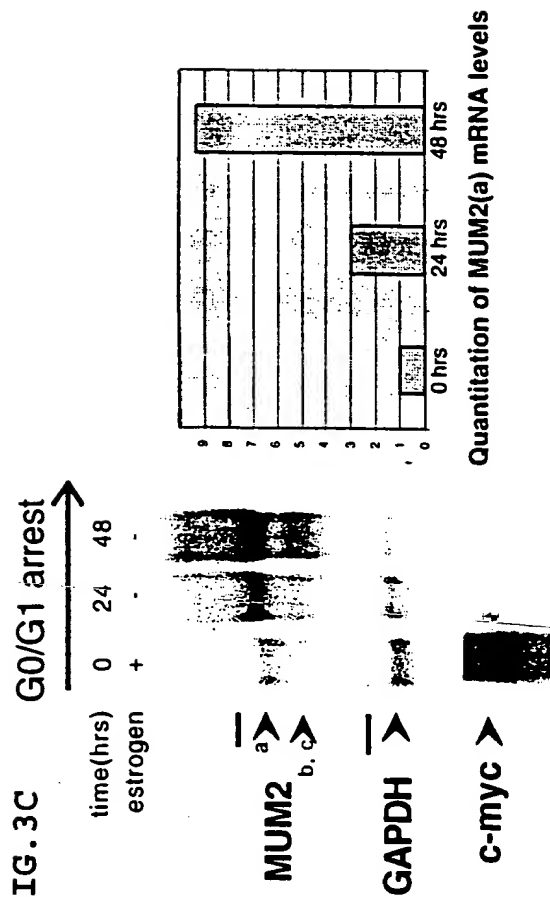


FIGURE 4

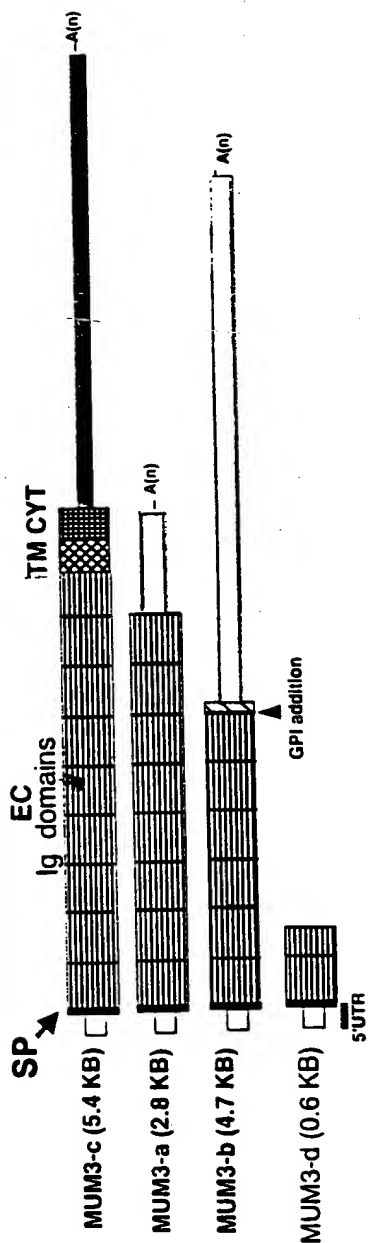


FIG. 4A

FIG. 4B

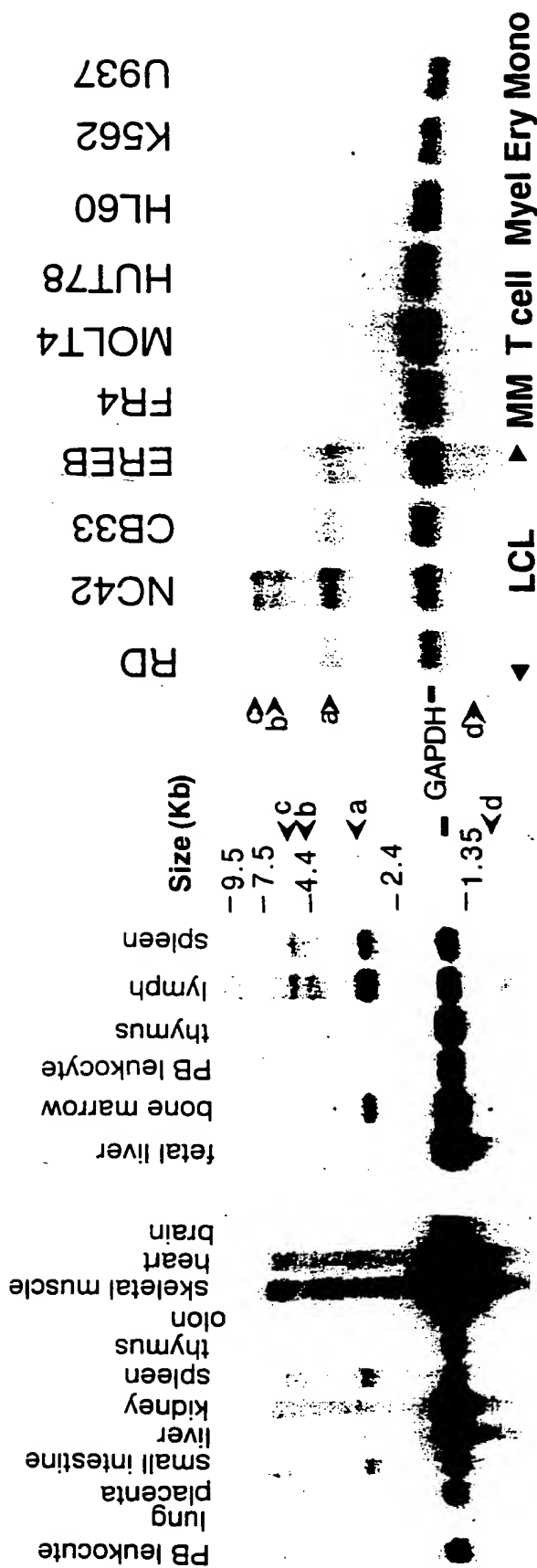


FIGURE 5

1 CTCAATCAGCTTTATGCAGAGAAGAAGCTTACTGAGCTCACTGCTGGTGGTGGTGTAGGCAAGTCTGCTTTGGCAA  
 78 TCTGGGCTGACCTGGCTTGTCTCCTCAGAACTCCTTCTCCAACCCTGGAGCAGGCTTCCATGCTGCTGTGGGCGTCC  
 155 TTGCTGGCCTTTGCTCCAGTCTGTGGACAATCTGCAGCTGCACACAAACCTGTGATTTCCGTCCATCCTCCATGGAC  
 232 CACATTCTTCAAAGGAGAGAGAGTGACTCTGACTTGAATGGATTTCAGTTCTATGCAACAGAGAAAACAATGGT  
 309 ATCATCGGCACTACTGGGGAGAAAAGTTGACCCTGACCCAGGAAACACCCTCGAGGTTGCGGAATCTGGACTGTAC  
 386 AGATGCCAGGCCCGGGCTCCCCACGAAGTAACCCTGTGCGCTTGTCTTTTCTTCAGACTCCTTAATCCTGCAGGC  
 463 ACCATATTCTGTGTTTGAAGGTGACACATTTGTTCTGAGATGCCACAGAAGAAGGAAAGAGAAATTGACTGCTGTGA  
 540 AATATACTTGAATGGAACATTTCTTTCCATTTCTAATAAAGCTGGGATCTTCTTATCCACAAGCAAGTTCAAAT  
 617 AACAATGGCAATTATCGATGCATTGGATATGGAGATGAGAATGATGATTTAGATCAAATTTCAAATAATTAAAT  
 694 TCAAGAACTATTTCCACATCCAGAGCTGAAAGCTACAGACTCTCAGCCTACAGAGGGGAATTCTGTAAACCTGAGCT  
 771 GTGAACACAGCTTCTCCAGAGCGGTGAGACACCCCACTTCACTTCAACTTCTTCAGAGATGGCGAGGTATCCTG  
 848 TCAGACTGGAGCAGTACCCGGAACCTCAGCTCCCAACCGTCTGGAGAGAAAACCTCAGGATCCTATTGGTGTGGTGC  
 925 TGAACAGTGAGGGTAACATCCACAAGCACAGTCCCTCGCTACAGATCCATGTGCAGCGGATCCCTGTGTCTGGGG  
 1002 TGCTCCTGGAGACCCAGCCCTCAGGGGGCCAGGCTGTTGAAGGGGAGATGCTGGTCTTGTCTGCTCCGTGGCTGAA  
 1079 GGCACAGGGGATACCATTTCTCTGGCAGGAGAGGATGCAGGAGAGTCTGGGGAGGAAAACCTCAGCGTTCCCT  
 1156 GAGAGCAGAGCTGGAGCTCCCTGCCATCAGACAGAGCCATGCAGGGGGATACTACTGTACAGACNAAACAGTACG  
 1233 GCCCTGTCCAGAGCATGGTGTGAATGTCACTGTGAGAGAGACCCCAAGCAACAGAGATGGCCTTGTGCGCCGCGGGA  
 1310 GCCACTGGAGGGCTGCTCAGTCTTCTCTGGCTGTGGCCCTGCTGTTTCACTGCTGGCTGGAGGAAGTCAGG  
 1387 AGTTGGTTTCTTGGGAGACGAAACCAGGCTCCCTCCCGCTCCAGGCCAGGAGAGTCTCCCATTCATCTGCCCTG  
 1464 CCCAGGTGGAGCTTCAGTCGTGTATGTTGATGTACACCCCAAAAGGGAGATTGGTATACTCTGAGATCCAGACT  
 1541 ACTCAGCTGGGAGAAGAAGAGGAAGCTAATACCTCCAGGACACTTCTAGAGGATAAGGATGTCTCAGTTGTCTACTC  
 1618 TGAGGTAAAGACACAACACCCAGATAACTCAGCTGGAAGATCAGCTCTAAGGATGAAGAAAGTTAAGAGAATGAAA  
 1695 AGTTACGGGAACGTCTACTCATGTGATTTCTCCCTTGTCCAAAGTCCCAGGCCAGTGCAGTCTTGGCGCACCTG  
 1772 GAATGATCAACTCATTCCAGCTTTCTAATTTCTCATGCATATGCATTCACTCCAGGAATACTCATTGCTCTACT  
 1849 CTGATGTTGGGATGGAATGGCCTCTGAAAGACTTCACTAAATGACCAAGGATCCACAGTTAAGAGAAGACCCCTGTAG  
 1926 TATTGCTGTGGGCTGACCTAATGCATTCCCTAGGGTCTGCTTTAGAGAAGGGGGATAAAGAGAGAGAAGGACTGT  
 2003 TATGAAAAACAGAAGCACAAATTTTGGTGAATTGGGATTGTCAGAGATGAAAAAGACTGGGTGACCTGGATCTCTGC  
 2080 TTAATACATCTACAACCATTTGTCTCACTGGAGACTCACTTGCATCAGTTTGTGTTAACTGTGAGTGGCTGCACAGGCA  
 2157 CTGTGCAAAACAATGAAAAGCCCTTCACTTGCCTGCACAGCTTACACTGTGAGGATTCAGTTGCAGATTAAGAGAA  
 2234 CCCATCTGGAATGGTTTACAGAGAGAGGAATTTAAAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC  
 2311 GCTTCCAAAAGCAAATGATAATTATGTTAATGTCAATTAGTGACAAAGATTGCAACATTAGAGAAAAGAGACACAAA  
 2388 TATAAAATTAATAAATTAAGTACCAACTCTCCAAAATAAATTGAACCTAAAATATTAGTATAAACTCATAATAAA  
 2465 CTCTGCCTTTAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6a

1 CGGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTTGGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTG  
     M L L W V I L L V L A P V S G Q F A R T P R 22  
 81 GTGGTCCAGGTCTTCATGCTGCTGTGGGTGATATTACTGGTCTGGCTCCTGTGAGTGGACAGTTTGCAAGGACACCCAG  
     P I I F L Q P P W T T V F Q G E R V T L T C K G F R F 49  
 161 GCCCATTATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTACCCTCACTTGCAAGGGATTTTCGCT  
     Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L 75  
 241 TCTACTCACACAGAAAACAAATGGTACCATCGGTACCTTGGGAAAAGAAATACTAAGAGAAAACCCAGACAATATCCTT  
     E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S 102  
 321 GAGGTTTCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTC  
     A S L I L Q A P L S V F E G D S V V L R C R A K A E V129  
 401 AGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAG  
     T L N N T I Y K N D N V L A F L N K R T D F H I P H 155  
 481 TAACACTGAATAATACTATTTACAAGAATGATAATGCTCTGGCATTCTTAATAAAAGAACTGACTTCCATATTCCTCAT  
     A C L K D N G A Y R C T G Y K E S C C P V S S N T V K 182  
 561 GCATGTCTCAAGGACAATGGTGCATATCGTGTACTGGATATAAGGAAAGTTGTGCCCTGTTTCTTCCAATACAGTKAA  
     I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L209  
 641 AATCCAAGTCCAAGAGCCATTTACACGTCCAGTGTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC  
     T C E T Q L S L E R S D V P L R F R F F R D D Q T L 235  
 721 TGACCTGTGAGACCCAGCTCTCTAGAGAGGTGAGATGTCCCGCTCCGGTTCGGCTTCTTTCAGAGATGACCAACCCCTG  
     G L G W S L S P N F Q I T A M W S K D S G F Y W C K A 262  
 801 GGATTAGGCTGGAGTCTCTCCCCGAATTTCCAGATTACTGCCATGTGGAGTAAAGATTGAGGTTCTACTGGTGTAAAGGC  
     A T M P H S V I S D S P R S W I Q V Q I P A S H P V L289  
 881 AGCAACAATGCCTCACAGCGTCATATCTGACAGCCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCC  
     T L S P E K A L N F E G T K V T L H C E T Q E D S L 315  
 961 TCACTCTCAGCCCTGAAAAGGCTCTGAATTTTGAAGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG  
     R T L Y R F Y H E G V P L R H K S V R C E R G A S I S 342  
 1041 CGCACTTTGTACAGGTTTTATCATGAGGTGTCCCCCTGAGGCACAAGTCAGTCCGCTGTGAAAGGGGAGCATCCATCAG  
     F S L T T E N S G N Y Y C T A D N G L G A K P S K A V369  
 1121 CTTCTCACTGACTACAGAGAATTCAGGGAATCTACTGACAGCTGACAATGGCCTTGGCGCCAAGCCAGTAAGGCTG  
     S L S V T V P V S H P V L N L S S P E D L I F E G A 395  
 1201 TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTGTCTCAACCTCAGCTCTCTGAGGACCTGATTTTTGAGGGAGCC  
     K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E 422  
 1281 AAGGTGACACTTCACTGTGAAGCCCAGAGAGGTTCACTCCCCATCCTGTACCAGTTTCATCATGAGGATGCTGCCCTGGA  
     R R S A N S A G G V A I S F S L T A E H S G N Y Y C T449  
 1361 GCGTAGGTCCGCCAATCTGCAGGAGGTGGCCATCAGTTCTCTGACTGCAGAGCATTGAGGAACTACTACTGCA  
     A D N G F G P Q R S K A V S L S I T V P V S H P V L 475  
 1441 CAGCTGACAATGGCTTTGGCCCCCAGCGCAGTAAGGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCTGTCTCTC  
     T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502  
 1521 ACCCTCAGCTCTGTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA  
     I L Y Q F Y H E D M P L W S S S T P S V G R V S F S529  
 1601 AATCCTATACCAGTTTTATCATGAGGACATGCCCCCTGTGGAGCAGCTCAACACCCTCTGTGGGAAGAGTGTCTTCACTG  
     S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555  
 1681 TCTCTCTGACTGAAGGACATTGAGGGAATTACTACTGCACAGCTGACAATGGCTTTGGTCCCCAGCGCAGTGAAGTGGTG  
     S L F V T V P V S R P I L T L R V P R A Q A V G D L 582  
 1761 AGCCTTTTGTCACTGTTCCAGTGCTCGCCCATCCTCACCCTCAGGGTTCCAGGGCCAGGCTGTGGTGGGGGACCT  
     L E L H C E A P R G S P P I L Y W F Y H E D V T L G 5609  
 1841 GCTGGAGCTTCACTGTGAGGCCCCGAGAGGCTCTCCCCAATCCTGTACTGGTTTTATCATGAGGATGTCACCCTGGGGA  
     S S A P S G G E A S F N L S L T A E H S G N Y S C E 635  
 1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTTCAACCTCTCTGACTGCAGAACATTCTGGAACACTACTCATGTGAG  
     A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662  
 2001 GCCAACAATGGCCTAGTGGCCAGCAGTGACACAATATCACTCAGTGTATAGTTCCAGTATCTCGTCCCATCCTCAC  
     F R A P R A Q A V V G D L L E L H C E A L R G S S P I689  
 2081 CTTTCAGGGCTCCCAGGGCCCAGGCTGTGGTGGGGGACCTGCTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA  
     L Y W F Y H E D V T L G K I S A P S G G G A S F N L 715  
 2161 TCCTGTACTGGTTTTATCATGAAGATGTCACCCTGGGTAAGATCTCAGGCCCTCTGGAGGAGGGCCCTCCTTCAACCTC  
     S L T E H S G I Y S C E A D N G L E A Q R S E M V T 742  
 2241 TCTCTGACTACAGAATCTGGAATCTACTCCTGTGAGGCAGACAATGGTCTGGAGGCCAGCGCAGTGAGATGGTGAC  
     L K V A G E W A L P T S S T S E N \* 759  
 2321 ACTGAAAGTTGCAGGTGAGTGGGCCCTGCCACCAGCAGCACATCTGGAACCTGACTGTGCCTGTTCTCCTGCAGCTGA  
 2401 AAATGGAGCCACAGAGCTCCTCAGGGCTGTTTGTGTGTGGCATCCAGCACACTTCTGCCTGCAGAACCTCCTGTG  
 2481 AAAGTCTCGGATCCTTTGTGGTATGGTTCCAGGAATCTGATGTTTCCAGCAGTCTTCTTGAAGATGATCAAAGCACCTC  
 2561 ACTAAAAATGCAATAAGACTTTTTTGAACATAAACTATATTCTGAACTGAAATTATTACATGAAATGAAACCAAGA  
 2641 ATTCTGAGCATATGTTTCTGTCCGTAGAAAGGATTAAGCTGTTTCTGTCCGATTCTTCTCATTGACTTCTAAGAA  
 2721 GCCTCTACTCTTGAGTCTCTTTCATTAAGGATGTAATGTTCTTACATTTCACATTAATAATCCTATGTTAACGA  
 AAAAA

FIGURE 6b

1 CGGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTTGGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTG  
 81 GTGGTCCAGGTCTTCACTGCTGTGGGTGATATTACTGGTCTCGGTCTCTGTCAGTGGACAGTTTGGCAAGGACACCCAG 22  
 P I I F L Q P P W T T V F Q G E R V T L T C K G F R F 49  
 161 GCCCATTATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGAAGGGATTTCGCT  
 Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L 75  
 241 TCTACTCACCACAGAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT  
 E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S 102  
 321 GAGGTTCAAGAACTGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACITGGATTTTCTTC  
 A S L I L Q A P L S V F E G D S V V L R C R A K A E V 129  
 401 AGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAGCGGAAG  
 T L N N T I Y K N D N V L A F L N K R T D F H I P H 155  
 481 TAACACTGAATAATACTATTACAAGATGATAATGCTCTGGCATTCTTAAATAAAGAACTGACTTCCATATTCCTCAT  
 A C L K D N G A Y R C T G Y K E S C C P V S N T K V K 182  
 561 GCATGTCTCAAGGACAATGGTGCATATCGCTGTACTGGATATAAGGAAAGTTGTTGCCCTGTTTCTTCCAATACAGTCAA  
 I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L 209  
 641 AATCCAAGTCCAAGAGCCATTTACAGCTCCAGTCTGAGAGCCAGCTCTTCCAGCCCATCAGCGGGAACCCAGTGACCC  
 T C E T Q L S L E R S D V P L R F R F R D D Q T L 235  
 721 TGACCTGTGAGACCCAGCTCTCTAGAGAGGTGAGATGTCCCGTCCGGTCCGGTCTTCTCAGAGATGACCAGACCCGTG  
 G L G W S L S Q I T A M W S K D S G F Y W C K A 262  
 801 GGATTAGGCTGGAGTCTCTCCCGAATTTCAGATTACTGCCATGTGGAGTAAAGATTGAGGGTCTTACTGGTGAAGGC  
 A T M P H S V I S D S P R S W I Q V Q I P A S H P V L 289  
 881 AGCAACAATGCCTCAGCGCTCATATCTGACGCGCCGAGATCCTGGATACAGGTGAGATCCCTGCATCTCATCTCTCC  
 T L S P E K A L N F E G G T K V T L H C E T Q E D S L 315  
 961 TCACTCTCAGCCCTGAAAAGGCTCTGAATTTGAGGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG  
 R T L Y R F Y H E G V P L R H K S V R C E R G A S I S 342  
 1041 CGCACTTTGTACAGGTTTATCATGAGGTGTCCCGCTGAGGCAAGTCAAGTCCGCTGTGAAAGGGGAGCATCCATCAG  
 F S L T T E N S G N Y Y C T A D N G L G A K P S K A V 369  
 1121 CTTCTCACTGACTACAGAGAATTCAAGGAACTACTACTGCACAGCTGACAATGGCCTTGGCGCCAAGCCAGTAAGGCTG  
 S L S V T V P V S L N L S S P E D L I F E G A 395  
 1201 TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTGTCTCAACCTCAGCTCTCCTGAGGACCTGATTTTGGAGGAGCC  
 K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E 422  
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 R R S A N S A G V A I S F S L T A E H S G N Y C T 449  
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 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475  
 1441 CAGCTGACAATGGCTTTGGCCCGCAGTAAAGCGGTGAGGCTCTCCATCACTGTCCTGTGTCTCATCTCTGCTCTC  
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502  
 1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA  
 I L Y Q F Y H E D M P L H S S S T P S V G R V S F S F 529  
 1601 AATCCTATACAGTTTATCATGAGGACATGCCCTCTGAGGAGCCTCAACACCCCTCTGTGGGAAGAGTGTCTTCACTG  
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555  
 1681 TCTCTGACTGAAGGACATTCAAGGAATTACTACTGCACAGCTGACAATGGCTTTGGTCCCCAGCGCAGTGAAGTGGTG  
 S L F V T G K C W V L A S H P P L A E F S L T H S F K 582  
 1761 AGCCTTTTGTCACTGGTAAGTGTGGGTCTTGGCAGTCAACCCCTGGCTGAGTCTCTCTCAACCATTCCTTTAA  
 N L F A L S S F L P \* stop 592  
 1841 AAATCTGTTGCACTGTCCAGTTTCTCCCTCAACTTAATCCCTTCTTGGCTTCTCTCAACTAAGTCTGGG  
 1921 GTTTTCCGTACTCATAAGTCTGTGCTCAGCCAGACCCCTAAAACAGCTCAGTAGATTCCCAGCTTTTACCAATGAATT  
 2001 TATTATTGTATTTTCTCTCATTCCTTGTATGTTTCCAACAGTACGCCAATTTTCTTGATGCACGGAGCGTGTCTTACT  
 2081 TCTCTACGACATTACATATTAATCTAGCTACAAGCAGCTTATAGATAAATATTGGTCAAGACCTTAAATCTCCA  
 2161 AAGGATTTCCAATCTTATGGTAGATTGGGAGAAAGCTGCTGGTGAACAAAGGGGAAATGGCTCCCTAGGAACCAACTCC  
 2241 TCAAACTCTGGAGTTTTTATGATCCCTTGTTTTCAACCTGCTAAAATCAGTATCATTTTATTGTATTATTTAAAAAA  
 2321 ACTATTGTTGAAGTATGACATACATTCAAGAAACGTGTCAAATTTGTATGTGTACGATTGGTGTCTTTTAGGAGCTAA  
 2401 GTTGTCTCTGTTTTTACTTGAATCTTTGTTTATAGAAACTGGGGGAAAGTTTACTTTCTTTTTCAGAGAAGCAAAATGTA  
 2481 TGATAGAAAAATCTTGAGCTGATGTGTGACATGCCCCTAGCATAACTTGTGAGTAAAGAGGTTATTTTAAATGT  
 2561 GAATGTTCTGAGACTACTCAAAGTCAGAGCCAAATCTACTAGGAAGCTTCTAGACTTCACTCATCTGCATCCCATTC  
 2641 TACTTTTTTACCATGTTTACTTTCTCTCATATTTCAGAGCATCTTAAGCCTCTTATTTTCTGTTTCTGACTGTCA  
 2721 CCCTTAATGCCAGTAGAATGTAAGCTTCATGAGAACGAACTGCATCCATCTTGGTCTTCAACATCCCTGTGCTACT  
 2801 CAGTGTGTTGGCACACAGTAGGTCTCAGTCAACATTTGTAATTTAGTGGACAGATGATATGACAAGATGATAAGAGGGGA  
 2881 TTTAAAAAATCATCTAGCAAAGCCCAAGAGGAAAAAACAAGCTATTTAGAAATGAAATACCAATTTGAAGCAGTA  
 2961 AGAATAGATTGGATATCTTTGAAAACCATTAATTGAATGAAGAACCAATTTGAGAAAACATACAGAATGCAAGTAGAA  
 3041 AGATACAGAAATAAAGGCAAAAGTTATAATATGGAATCAGACAAATGGATTGTCTGTATCCAGTTATGTGGATAATTAA  
 3121 AATGGAGACCCCTCAGAAAATTGAACCGAAGAGTAAATGAAACTCAAAAATGTAGTAGAAATTTGTTGGGAAGTAAAGAAA  
 3201 ACTTGAATATGTAGATCAGAACATATATGTTGATGACGTTATTTGACTTTGAGGTTAAAAATATATATATGTGCTTATGAT  
 3281 TATGGGAAAAAAGCAGTCTGCTCAGAAAGAAAAACATCAAGTTAGTCTTAGACTTTGCACTGCACTCAGTACCAAGAG  
 3361 AGAGGAGGCCAGACTTGGACCTGCGAGGGAAGAATAATACCCGAAAAATTTATATCAATTCAAAAAGACATTGTCAAAAA  
 3441 TACAGGATTTCAGGAACTGAGAACTGACCTAAGCCTTCTGGAACCAACACCTAATGACAAAATCTAGCCCAACCAAGTGT  
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 3601 GACCTTTGTAAGAGGTACACATTCAGTCTCGTCAAGGCCCTCTCCAGACTAATTCAGTATCAGAAATCTCAGAGATGGGGCC  
 3681 ACAGAATCAGTATTTTGGACACAACCTCAAGTGAGAATTGTGTAGACAAGATTGGAACCACTGATTGTAGATATAGA  
 3761 AACAAAGGCTAATCAACTGTGAGAATTATGGTACAGAATAGAAAGTAACATTATGAACACTGAAAATGTAAAAAAT  
 3841 GTAACAAAGAAAAATAGTTAGAGGAAGGAGAGGAGTAAAGGAACAATCATTTTCTCATGATTATTATTATTCAGAGTA  
 3921 AATTGTGAGTTATTTCAATTCAAAAAGATGGACTTTTTAAAAAATTAGTAATAGATTTCAAAAATGTCCATTTTGTA  
 4001 AATCGTTTCTGAATACTTTGTCAACAGTTACTCATATTAATGGCTTACTTCACTAAAATTCATGGAAAACCAACTA  
 4081 TAGCCTGTAGAGTACATAGGAGAGAACAAGTGAATCTTTGGGTGGCGCAAGCATAGATGTTAGGACTGACAAAAAA  
 4161 AATAATAAAAAATAAACCCTGTGCATTGATATGATCAAAATGATCAGGGAAGAGGAAACAGAAACTCTCATACGCCATTA  
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 4321 ATTTTGTATATACATACATGTTATATAACGATCAAATTAGGATATTTAATGTACCCATCATCTCATGCAATTTATCATTTCT  
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FIGURE 6c-1

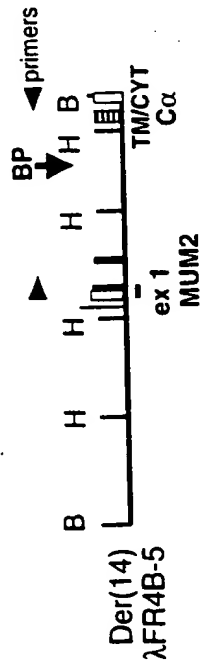
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 M L L W V I L L V L A P V S G Q F A R T P R 22  
 81 GTGGTCCAGGTCTCTCATGCTGTGGGTGATATTACTGGTCTGGCTCCTGTCTAGTGGACAGTTTGCAAGGACACCCAG  
 P I I F L Q P P W T T V F Q G E R V T L T C K G F R F 49  
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 241 TCTACTCACCACAGAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT  
 E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S 102  
 321 GAGGTTGAGGAATCTGGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCAGTTGGATTTCCTTC  
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 401 AGCTTCGCTGATCTGCAAGCTCCACTTTCTGTGTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAG  
 T L N N T I Y K N D N V L A F L N K R T D F H I P H 155  
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 641 AATCCAAGTCCAAGAGCCATTTACACGTCCAGTGTCTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC  
 T C E T Q L S L E R S D V P L R F R F R F R D L 235  
 721 TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTGAGATGTCCCGCTCCGGTTCGCTTCTTCTAGAGATGACCAGACCTG  
 G L G W S L S P N F Q I T A M W S K D S G F Y W C K A 262  
 801 GGATTAGGTGGAGTCTCTCCCGAATTTCCAGATTAAGTGTGAGTAAAGATTGAGGTTCTAGTGGTGAAGGC  
 A T M P H S V I S D S P R S W I Q V Q I P A S H P V L 289  
 881 AGCAACAATGCCTCACAGCGTCATATCTGACAGCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTCTCC  
 T L S P E K A L N F E G T K V T L H C E T Q E D S L 315  
 961 TCACTCTCAGCCCTGAAAAGGCTCTGAATTTGAGGGAACCAAGGTGACACTTCACTGTGAACCCAGGAAGATTCTCTG  
 R T L Y R F Y H E G V P L R H K S V R C E R G A S I S 342  
 1041 CGCATTGTTTACAGGTTTTATCATGAGGGTGTCCCTTGAAGGCAAGTCAGTCCGCTGTGAAAGGGGAGCATCCATCAG  
 F S L T T E N S G N Y Y C T A D N G L G A K P S K A V 369  
 1121 CTTCTCACTGACTACAGAGAATTCAGGGAACCTACTGTCACAGCTGACAATGGCCTTGGCGCCAAGCCAGTAAGGCTG  
 S L S V T V P V S H P V L N L S S P E D L I F E G A 395  
 1201 TGAGCCTCTCAGTCACTGTCTCCCGTGTCTCATCTGCTCAACCTCAGCTCTCTGAGGACCTGATTTTGAAGGAGCC  
 K V T L H C E A Q R G S L P I L Y Q F H E D A A L E 422  
 1281 AAGGTGACACTTCACTGTGAAGCCAGAGAGGTCACTCCCATCTGTACAGTTTCATCATGAGGATGCTGCCCTGGA  
 R R S A N S A G G V A I S F S L T A E H S G N Y Y C T 449  
 1361 GCGTAGGTCGCGCAACTCTGAGGAGGAGTGCCCATCAGCTTCTCTGACTGCAGAGCATTGAGGGAACCTACTGCA  
 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475  
 1441 CAGCTGACAATGGCTTTGGCCCCAGCGCAGTAAGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCTGTCTC  
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502  
 1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA  
 I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F 529  
 1601 AATCTATACAGTTTATCATGAGGACATGCCCTGTGAGCAGTCAACACCCTCTGTGGGAAGAGTGTCTCAGCT  
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555  
 1681 TCTCTCTGACTGAAGGACATTGAGGAATTAAGTGTGACAGCTGACAATGGCTTTGGTCCCAGCGCAGTGAAGTGGTG  
 S L F V T V P V S R P I L T L R V P R A Q A V V G D L 582  
 1761 AGCCTTTTGTCACTGTTCCAGTGTCTCGCCCCATCTCACCCTCAGGGTCCCAGGGCCAGGCTGTGGTGGGGGACCT  
 L E L H C E A P R G S P P I L Y W F Y H E D V T L G S 609  
 1841 GCTGGAGCTTCACTGTGAGGCCCGAGAGGCTCTCCCCAATCTGTACTGGTGTATCATGAGGATGTCAACCTGGGGA  
 S S A P S G G A S F H L T A E H S G N Y S C E 635  
 1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTCAACCTCTCTGACTGCAGAACATTCTGGAACCTACTCATGTGAG  
 A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662  
 2001 GCCAACATGGCCTAGTGGCCAGCAGTGACACATATCACTCAGTGTATAGTTCCAGTATCTGCTCCCATCTCAC  
 F R A P R A Q A V V G D L L E L H C E A L R G S S P I 689  
 2081 CTTCAAGGCTCCCAGGGCCAGGCTGTGGTGGGGGACCTGCTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA  
 L Y W F Y H E D V T L G K I S A P S G G G A S F N L 715  
 2161 TCTGTACTGGTTTTATCATGAAGATGTCAACCTGGGTAAAGATCTCAGCCCCCTCTGGAGGAGGGCCCTCTCAACCTC  
 S L T T E H S G I Y S C E A D N G L E A Q R S E M V T 742  
 2241 TCTCTGACTACAGAACATTCTGGAATCTACTCTGTGAGGCAGACAATGGTCTGGAGGCCAGCGCAGTGAGATGGTGAC  
 L K V A V P V S R P V L T L R A P G T H A A V G D L L 769  
 2321 ACTGAAAGTTGCAAGTCCGGTGTCTCGCCCGGTCTCACCCTCAGGGCTCCCGGGACCATGTCTCGGTGGGGGACCTGC  
 E L H C E A L R G S P L I L Y R F F H E D V T L G N 795  
 2401 TGGAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCCTGATCTGTACCGGTTTTTTCATGAGGATGTCAACCTAGGAAAT  
 R S S T P S G G A S L N L S L T A E H S G N Y S C E A D 822  
 2481 AGGTCTGCCCCCTCTGGAGGAGCGTCTTAAACCTCTCTGACTGCAGAGCACTCTGGAACCTACTCTGTGAGGCCGA  
 N G L G A Q R S E T V T L Y I T G L T A N R S G P F A 849  
 2561 CAATGGCCTCGGGGCCAGTCAGTGAGACACTTTATATCAGGGCTGACCGGAGAGGAGTGTGAGGCTTTTGT  
 T G V A G G G L L S I A G L A A G A L L Y C W I S R 875  
 2641 CCACAGGAGTCCGCGGGGGCTGTCTCAGCATAGCAGGCTTCTGCGGGGGCACTGCTGCTCTACTGCTGCTCTCGAGA  
 K A G R K P A S D P A R S P S D S D S Q E P T Y H N V 902  
 2721 AAAGCAGGGAGAAAGCCTGCCTCTGACCCCGCCAGGAGCCCTTCACTCGGACTCCCAAGAGCCCACTATCACAATGT  
 P A W E E L Q P V Y T N A N P R G E N V V Y S E V R I 929  
 2801 ACCAGCTGGGAAGAGTGAACCAAGTGTACTAATGCAATCTAGAGGAGAAATGTGTTTACTCAGAAGTACGGA  
 I Q E K K K H A V A S D P R H L R N K G S P I I Y S 955  
 2881 TCATCCAAGAGAAAAAGAACATGCAGTGGCCTCTGACCCAGGCATCTCAGGAACAAGGGTTCCCTATCATCTACTCT

## FIGURE 6c-2

E V K V A S T P V S G S L F L A S S A P H R \* stop 977

2961 GAAGTTAAGGTGGCGTCAACCCCGGTTTCCGGATCCCTGTTCTTGGCTTCCTCAGCTCCTCACAGATGAGTCCACACGTC  
3041 TCTCCAACCTGCTGTTTCAGCCTCTGCACCCCAAAGTTCCTTGGGGGAGAAGCAGCATTGAAGTGGGAAGATTAGGCT  
3121 GCCCCAGACCATATCTACTGGCCTTTGTTTCACATGTCTCATTCTCAGTCTGACCAGAATGCAGGGCCCTGCTGGACTG  
3201 TCACCTGTTTCCAGTTAAAGCCCTGACTGGCAGGTTTTTTAATCCAGTGGCAAGGTGCTCCCACTCCAGGGCCAGCAC  
3281 ATCTCCTGGATTCTTAGTGGGCTTCAGCTGTGGTGTCTGTTCTGAGTACTGCTCTCATCACACCCCCACAGAGGGGGTTC  
3361 TTACCACACAAAGGGAGAGTGGGCTTCAGGAGATGCCGGGCTGGCCTAACAGCTCAGGTGCTCCTAACTCCGACACAG  
3441 AGTTCCTGCTTTGGGTGGATGCATTCTCAATTGTCATCAGCCTGGTGGGGCTACTGCAGTGTGCTGCCAAATGGGACAG  
3521 CACACAGCCTGTGCACATGGGACATGTGATGGGTCTCCCCAGGGGGCTGCATTTACACTCCTCCACCTGTCTCAAACCT  
3601 CTAAGGTCGGCACTTGACACCAAGGTAACCTCTCTCTGCTCATGTGTGCTAGTGTCTACCTGCCCAAGTAAGTGGCTTTCA  
3681 TACACCAAGTCCCGAAGTTCTTCCCATCCTAACAGAAGTAACCCAGCAAGTCAAGGCCAGGAGGACCAGGGGTGCAGACA  
3761 GAACACATACTGGAACACAGGAGGTGCTCAATTACTATTTGACTGACTGACTGAATGAATGAATGAATGAGGAAGAAAAC  
3841 TGTGGGTAAATCAAACCTGGCATAAAATCCAGTGCCTCCCTAGGAAATCCGGGAGGTATTCTGGCTTCCTAAGAAACAACG  
3921 GAAGAGAAGGAGCTTGGATGAAGAACTGTTTCAGCAAGAAGAAGGCTTCTTCACACTTTTATGTGCTTGTGGATCACCT  
4001 GAGGATCTGTGAAAAACAGATACTGATTGAGTGGGTCTGTGTAGAGCCTGAGACTGCCATTCTAACATGTTCCAGGGG  
4081 ATGCTGATGCTGTGCCCCCTGGGACTGCCTGCATGCATGTGAAGCCCTATAGGTCTCAGCAGAGGGCCATGGAGAGGGA  
4161 ATGTGTGGCTCTGGCTGCCAGGGCCCACTCGGTTTCACAGGATCGTGTGCTCCTCGGCCAGCCTTTGGCCACAGCAC  
4241 CACCAGCTGCTGTTGCTGAGAGAGCTTCTTCTCTGTGACATGTTGGCTTTCATCAGCCACCCTGGGAAGCGGAAAGTAGC  
4321 TGCCACTATCTTTGTTTCCCACTCAGGCCTCACACTTTCCCATGAAAAGGGTGAATGTATATAACCTGAGCCCTCTCC  
4401 ATTCAGAGTTGTTCTCCCATCTCTGAGCAATGGGATGTTCTGTTCCGCTTTTATGATATCCATCACATCTTATCTTGATC  
4481 TTTGCTCCCACTGGATTGTACAGTGATGACTTTTAAGCCCCACGGCCTGAAATAAAATCCTTCCAAGGGCATTGGAAGC  
4561 TCACTCCACCTGAACCATGGCTTTTCATGCTTCAAGTGTGAGGGCCTTGCCAGATAGACAGGGCTGACTCTGCTGCCC  
4641 CAACCTTTCAAGGAGGAAACCAGACACCTGAGACAGGAGCCTGTATGCAGCCAGTGCAGCCTTGACAGGAGCAAGGCTG  
4721 GAGGCATTTGTCTACACTACAGATATGCAACTAAAATAGACGTGGAGCAAGAGAAATGCATTTCCACCGAGGCCGCTTTT  
4801 TTAGGCCCTAGTTGAAAGTCAAGAAGGACAGCAGCAAGCATAGGCTCAGGATTAAAGAAAAAAATCTGCTCACAGTCTGTT  
4881 CTGGAGGTACATCACCAACAAAGCTCACGCCCTATGCAGTCTGAGAAGGTGGAGGCACCAGGCTCAAAGAGGAAATT  
4961 TAGAATTTCTCATTGGGAGAGTAAGGTACCCCATCCAGAATGATAACTGCACAGTGGCAGAACAACTCCACCCTAAT  
5041 GTGGGTGGACCCCATCCAGTCTGTTGAAGGCTGAATGTAACAAAAGGGCTTATTCTTCTCAAGTAAGGGGGAATCCT  
5121 GCTTTGGGCTGGGACATAAGTTTTCTGCTTTTCAGACGCAAACTGAAAAATGGCTCTTCTTGGGTCTTGAGCTTGTGCGC  
5201 ATATGGACTGAAAGAACTATGCTATTGGATCTCCTGGATCTCCAGCTTGCTGACTGCAGATCTTGAGATATGTCAGCCT  
5281 CTACAGTCACAAGAGCTAATTCATTCTAATAAACCAATCTTTC

**FIG. 7A**



Probe: ex 1 MUM2

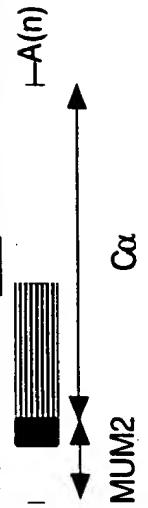
MUM2

EMB

U266

JUN3

FRA

[illegible]

12/34

FIGURE 8A

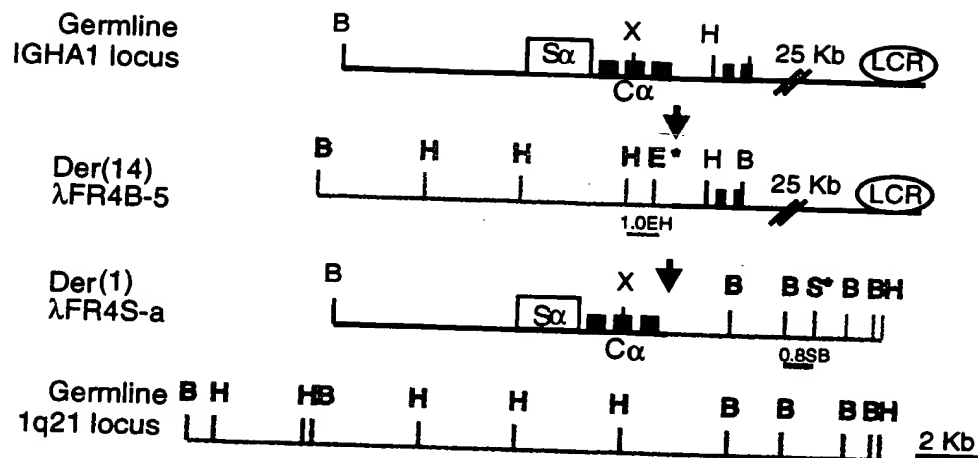


FIGURE 8

Chr 14 TCCCACTGACGCATGCAGGAAGGGGACCTCCCTTAAACACACTGCTCTGTACGGGGCACGTTGGGCACAGGTGCACACTCACA  
 Der (14) GGCCTGACAGCAACTTTCTTCTACTAGTTTCATCTTAA - CACACTGCTCTGTACGGGGCACGTTGGGCACAGGTGCACACTCACA  
 Chr 1 GGCCTGACAGCAACTTTCTTCTACTAGTTTCATCTTAACTTATCCTGGTAACTGGCGAGACAACCTGTCTTAAGTAACTGAAGGAAA  
 Chr 1 GGCCTGACAGCAACTTTCTTCTACTAGTTTCATCTTAACTTATCCTGGTAACTGGCGAGACAACCTGTCTTAAGTAACTGAAGGAAA  
 Der (1) TCCCACTGACGCA ----GGAAGGATCTTAAAGTTTATCCTGGTAACTGGCGAGACAACCTGTCTTAAGTAACTGAAGGAAA  
 Chr 14 TCCCACTGACGCATGCAGGAAGGGGACCTCCCTTAAACCACTGCTCTGTACGGGGCACGTTGGGCACAGGTGCACACTCACA

8c

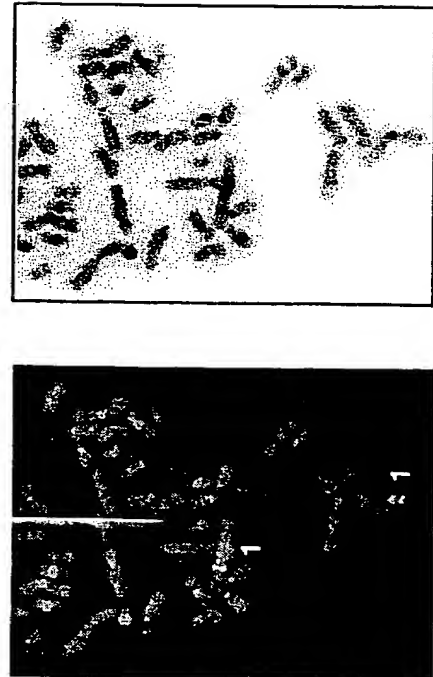


FIGURE 9

0.5 Kb

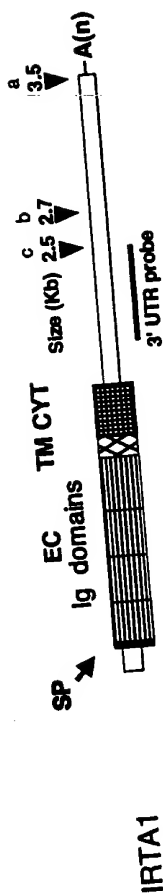


FIG. 9A

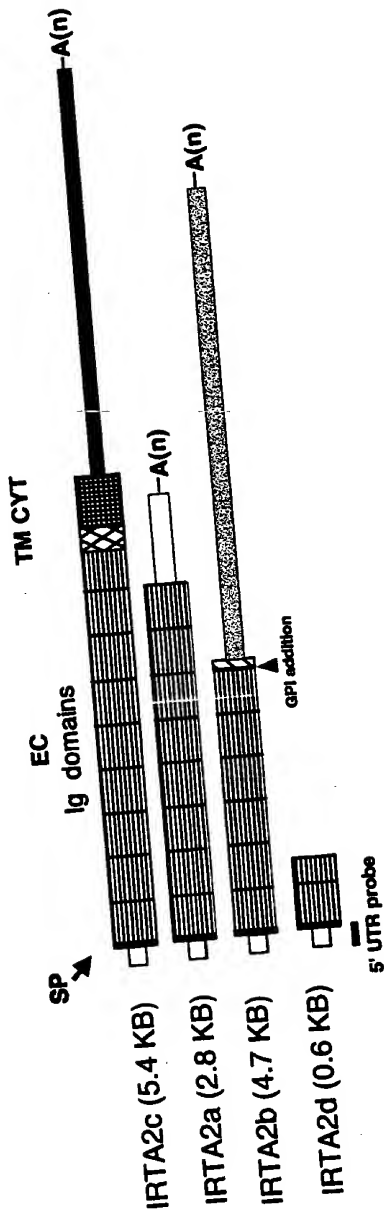


FIG. 9B

FIGURE 10

FIG. 10A

FCGR1IA (1) MAMETQMSQNVCPNWLQPTWVLLILIAADGCAAPFAAARLIPPIIADGQESVTHITVARSPEIDIOHFINKIIPHIQSYRPFKANNKX  
 FCGR1IA (1) -----SQWLLIFLALIAAGKEDTLPAWFLFQPYRWDKKEVTHKGLAYSPPNNSTQWFINEIICQSYFIDATVPEAK  
 FCER1A (1) -----MAP-AIESPTLCAADAPAPDFVLVPOQKESUNPPNRRSPKSENVTHITQNNFESSTRQPFHNCETISSTSLNINAKFDPK  
 FCGR1A (1) -----WQWALIAWPPVDEGV-DTNAVISLCPNVSVQCEAVTHITVVLHFGSTQWFLNATATSPYRITSASNDK  
 IRTA1 (1) -----KLWESLIAAPVCEGSAAARVIGVGPWTFKRTIRWTHITQNFQYAEVITVIMHYWCEILLPNGTI-LEQSEK  
 IRTA2 (1) -----HILWILIAAPVSGFARTPEZLIFQPPITVFOGRVTHITQNFREYEQTHVIRYLKILREPDNI-LEVQSEK

FCGR1IA (101) EYTCCTQSTEDVATVLEWVILQADHLEPQKESVWLRCHWKKPIKAVTAMONKQHSLETHLIPAAVHSSEPVATNNAYTL-SKK  
 FCGR1IA (86) EVKCCITLTTASDIVCDEVHIEMILLOARWVKEDITHRCHEKNNRTATKAVTHIQNGKRRSGHHQDEYILKMAKUSEFVTRRLKSKN-VEE  
 FCER1A (90) EVKCCHEOVNESEPVVEMFEMILLLOAQAAYVMEGCPINRCHQDQWDAKAVAKQCEELHSGVPLTSSIPATAVAREDEETATYCTERQMLD-22E  
 FCGR1A (82) EVKCCRLGGRDPRGLFETHREMLLQVSRVTEGEPPLIRCHAKWKLESAWVAYRNGRQKDKAMSSAYILKMAKSENGVCEERKKHR-22A  
 IRTA1 (82) LYRCCAGCPRENPAVGLFSSTSLLOAPYSVF-EGDAEDRCHRRREKTPAKVTVWNCNHLSESKWDILIPZASNNNGVYTIQYCEENDVREN  
 IRTA2 (82) EVRCCAGCPLESPPVHIFFSASLILQAPLSVF-EGDSASVQCEKAAVTDNAPVTK-NQNTLAPNKEDEHHPAAKQNGVTRCTYKESCCPVSEN

FCGR1A (172) EKHR--KTSACGSHTKKLEPAVIVASVMSIIEGNLVTSCTKLLQPLQLOTPESHMGSLD-RQNVSEZOILVTRPDYVWPAVIEDGN  
 IRTA1 (171) SEENDVFRSNFKIKIOLHHPLEKADQOE-TEGNSNMSCETCPPEHETPIKNTPRRQCEVLSDSITYELQVPTVRENKYSWCAETPRAN  
 IRTA2 (170) KESCCPSSNTTKIQVOPPTPRVIRASSFQE-ESNPVILAGTQISLESIMPIREREREDQIRGLSSILHINQOIZAMSKDERTWKAAVTPHS

FCGR1A (269) YKKEHIEERQVLCQPTWVWHLGYLAVKMFVAVVWVIRKEERKKKDEISLGHKKVTSLODRHEELKQOE-EKEQLQCEVH  
 IRTA1 (270) GHHEHISQIHQRIPVGVV-ETQISSEKAVECEVAVSVAEGGDTASVREDQESLARKQGLLHMLLEPQKQSHK-CVYDAINSY-  
 IRTA2 (269) VASDERSWLOVQ-IPASHV-ITLSPEKALNFECTKRVTHITQEDSIRTHYRTHEGV--PIRRHREVCERASISFSTTENEC-NVYCAADNMGCA

E E E I I I  
 DXXXXXXX--DXX--YXXLXXXXXXX--YXXL

ITAM:

IRTA1: ESSHISICPAQVHLQSLYVDVHPKKG-DLVYSEIQTTTLGEEEEEAANTSRTLLEDKDVSVVYSEV  
 PECAM: DNKEPLNSDVQYXTEVQVSSAEWSHK-----DLGKKDTEVYSEV  
 IRTA2C: DSDSQ---EPTXHNVPAAWEELQPVYT-----NANPRGENVYSEV  
 BGP1: ASDQR---DLTEHKPVSVNHTQDHSN-----DPPKNMNEVTYSTL

X<sup>(34)</sup> IIYSEVK  
 X<sup>(31)</sup> IIYSEVK

ITIM: SXXXXL SXXXXL SXXXXL  
 V V V  
 L L L  
 I I I

FIG. 10B

FIGURE 11A

11A

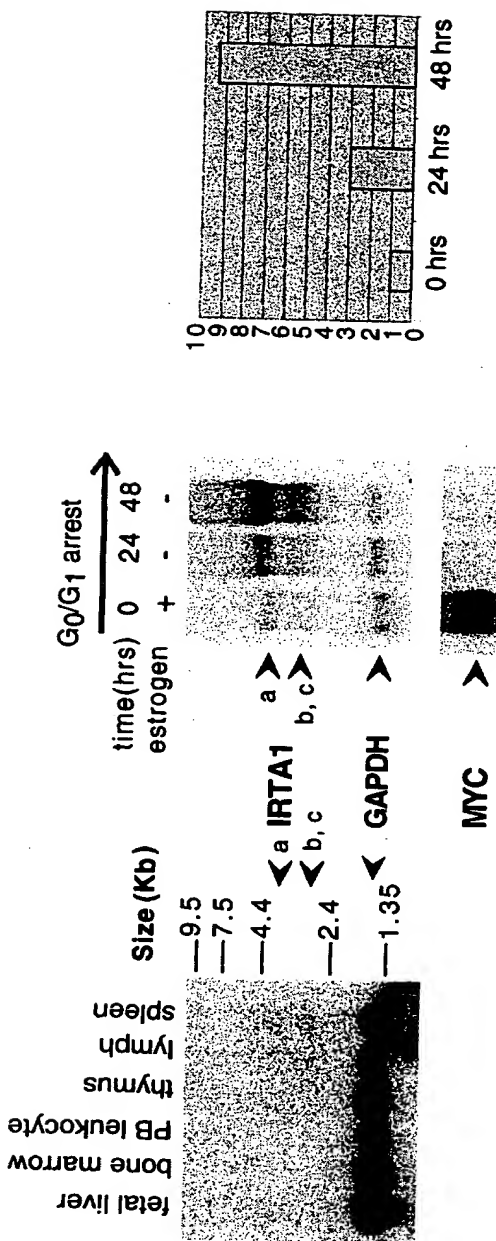




FIGURE 11B1-B4

11B1-4

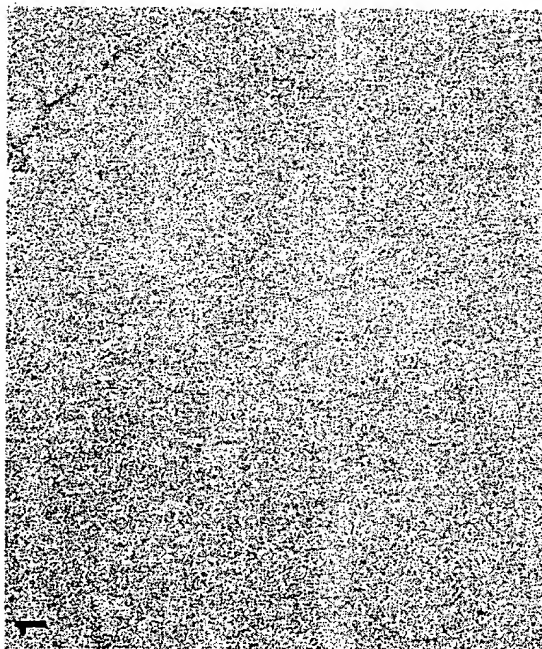
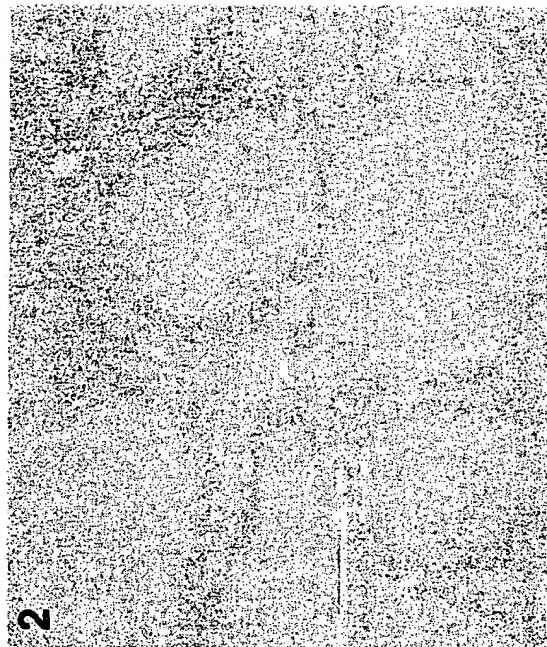
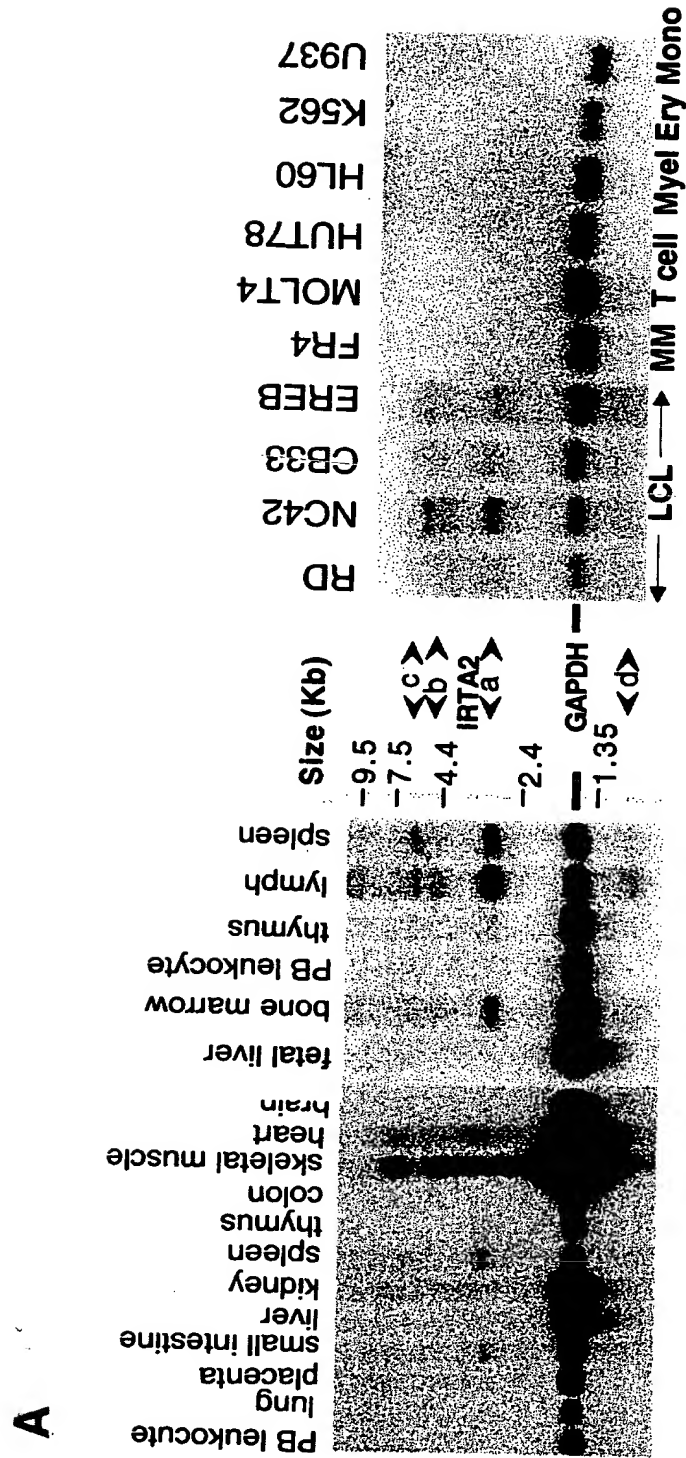
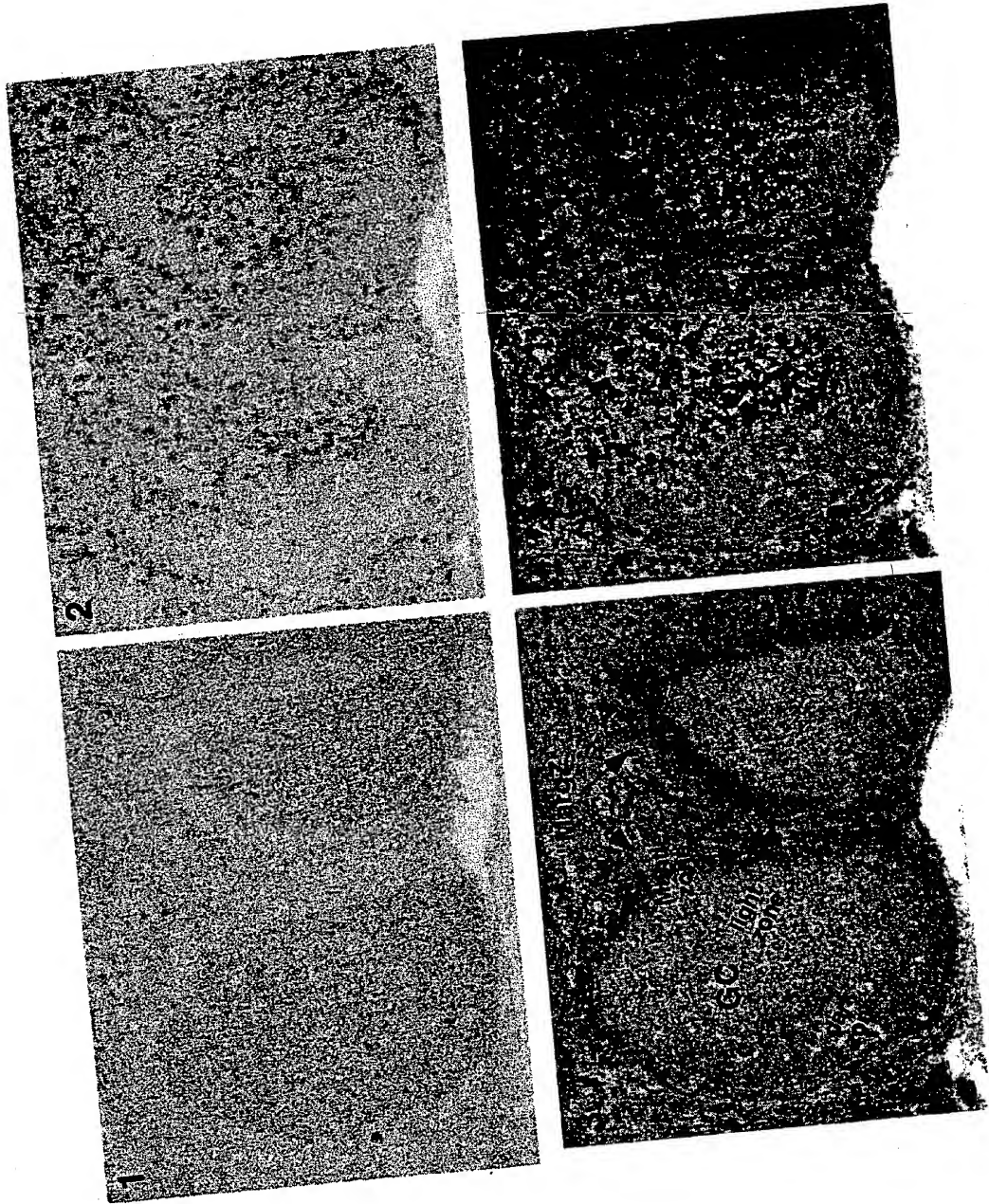


FIGURE 12A.



SECRET  
GROUP 1  
EXCLUDED FROM AUTOMATIC DOWNGRADING AND DECLASSIFICATION

FIGURE 12B1-B4



B

[illegible]

FIGURE 14

FIG. 14A

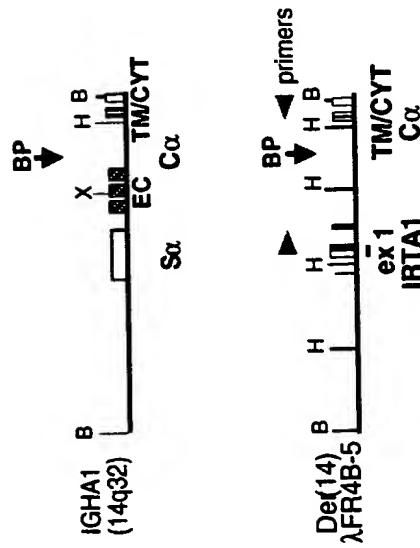


FIG. 14C

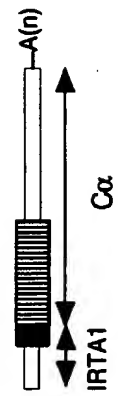


FIG. 14B

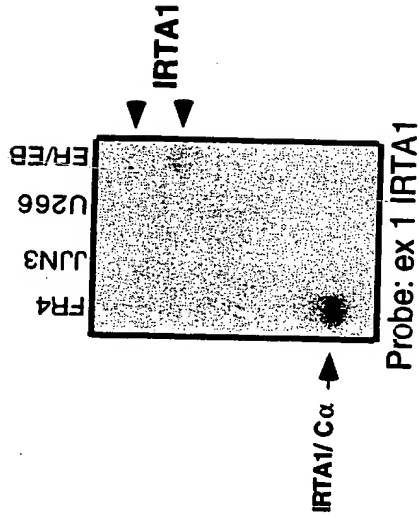


FIG. 14D

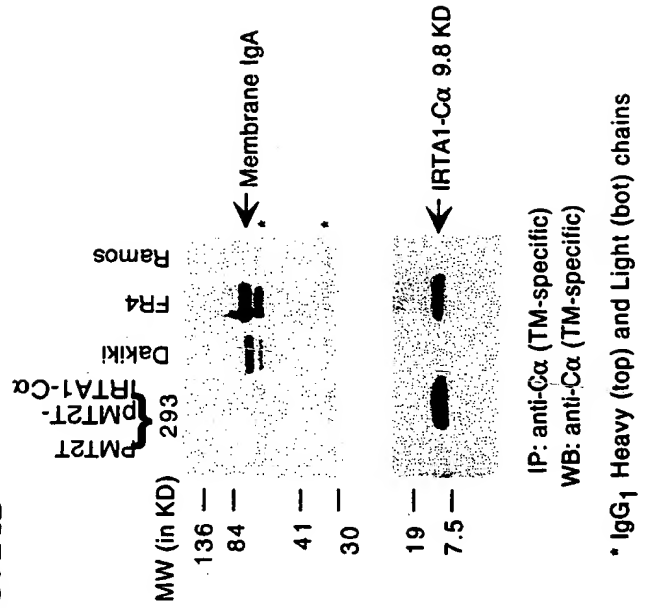


FIGURE 15

FIG.15A

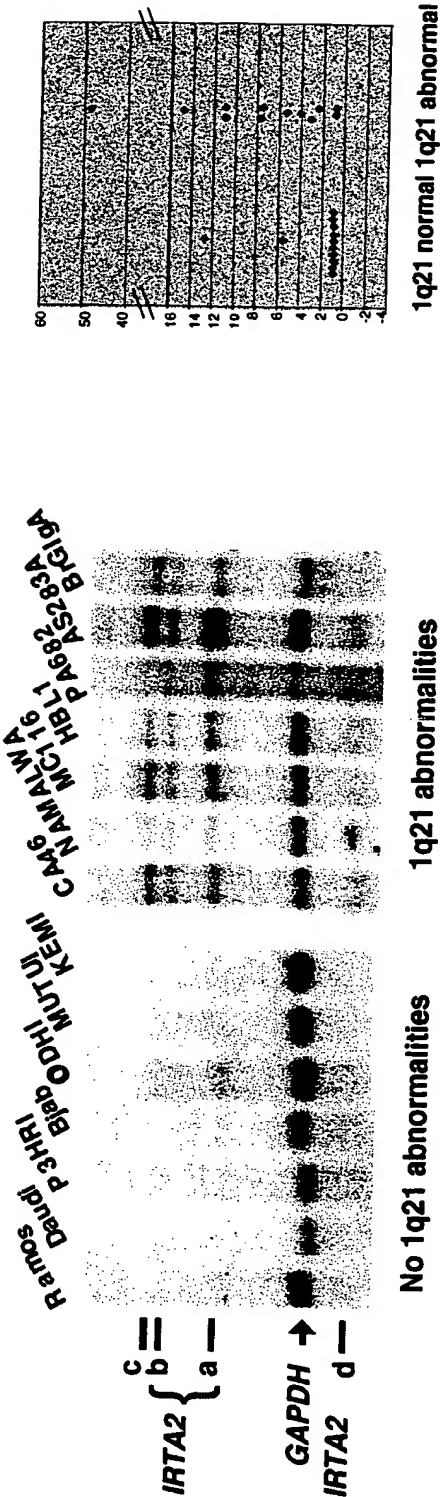
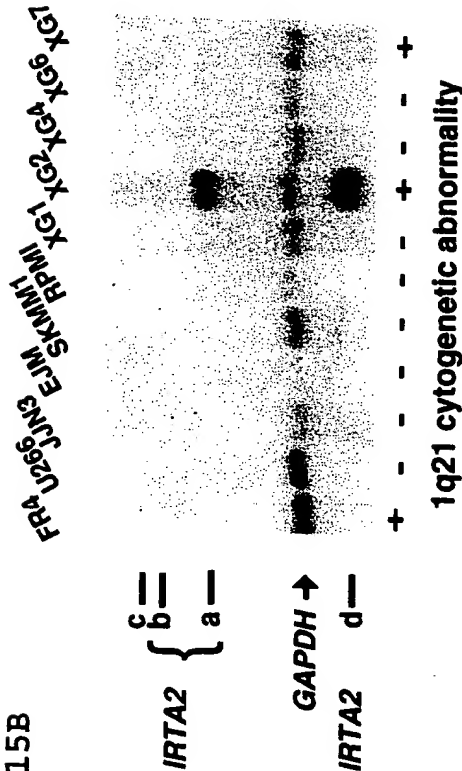


FIG.15B



Cell line	IRT A2
Burkitt Lymphoma	
Normal 1q21	2/12
Abnormal 1q21	10/12
Multiple Myeloma	
Normal 1q21	0/7
Abnormal 1q21	1/3

Summary of IRTA2 expression

FIGURE 16-1~16-4  
IRTA1 expression in normal lymphoid tissue





FIGURE 17

**IRTA1 expression in a stomach Mucosa-Associated-Lymphoid Tissue B cell lymphoma**

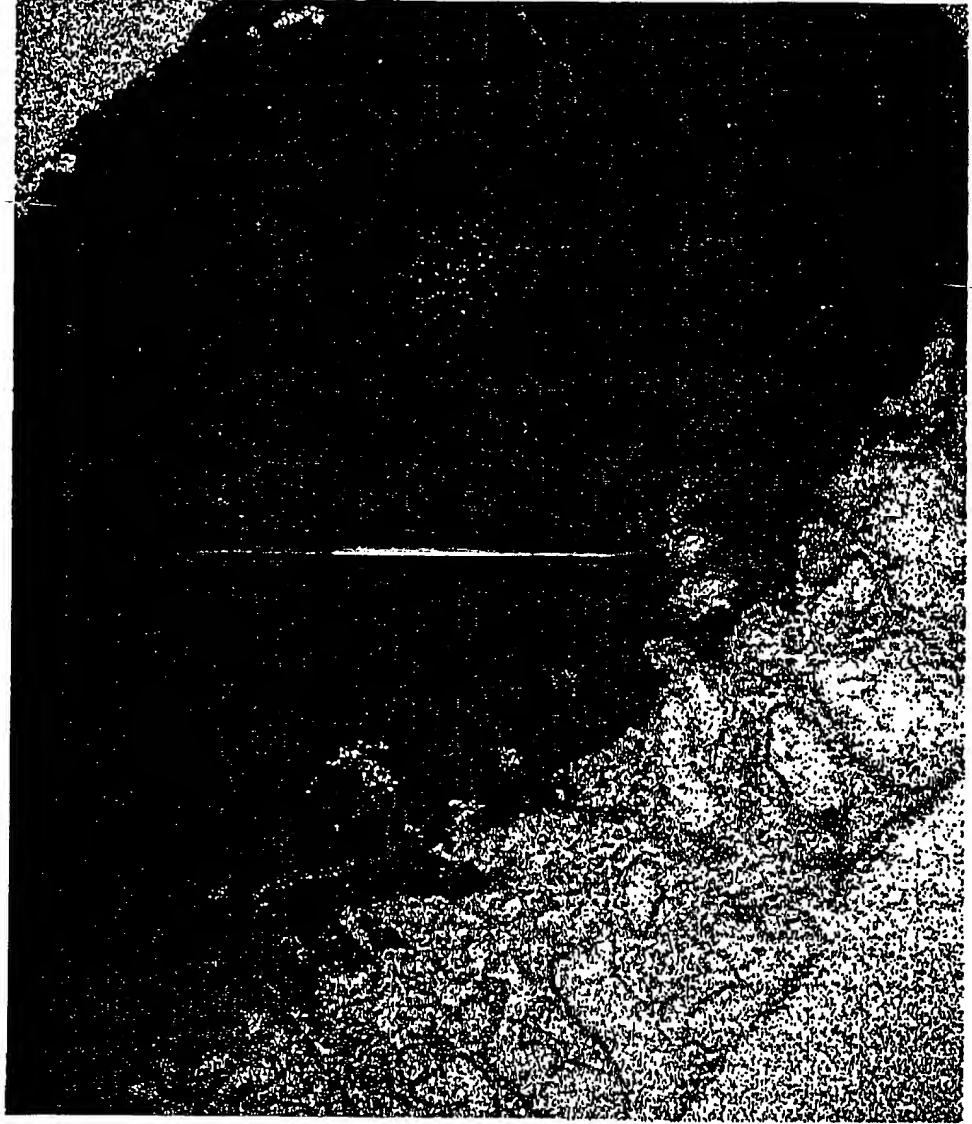




FIGURE 18A

1 CTCAATCAGCTTTATGCAGAGAAGAAGCTTACTGAGCTCACTGCTGGTGTGGTGTAGGCAAGTGCTGCTTTGGCAA  
 78 TCTGGGCTGACCTGGCTTGTCTCCTCAGAACTCCTTCTCCAACCTGGAGCAGGCTTCCATGCTGCTGGGCGTCC  
 L L A F A P V C G Q S A A A H K P V I S V H P P W T 32  
 155 TTGCTGGCCTTTGCTCCAGTCTGTGGACAATCTGCAGCTGCACACAAACCTGTGATTTCCGTCCATCCTCCATGGAC  
 T F F K G E R V T L T C N G F Q F Y A T E K T T W Y 58  
 232 CACATTCTTCAAAGGAGAGAGAGTGAAGTCTGACTTGAATGGATTTCAGTTCTATGCAACAGAGAAAACAACATGGT  
 H R H Y W G E K L T L T P G N T L E V R E S G L Y 83  
 309 ATCATCGGCACTACTGGGAGAAAAGTTGACCTGACCCAGGAAACACCTCGAGGTTCCGGGAATCTGGACTGTAC  
 R C Q A R G S P R S N P V R L L F S S D S L I L Q A 109  
 386 AGATGCCAGGCCCGGGCTCCCCACGAAGTAACCTGTGCGCTGCTCTTTCTTCAGACTCCTTAATCTGCAGGC  
 P Y S V F E G D T L V L R C H R R R K E K L T A V K 135  
 463 ACCATATTCTGTGTTTGAAGGTGACACATTGGTTCTGAGATGCCACAGAAGAAGGAAAGAAATGACTGCTGTGA  
 Y T W N G S I S N K S W D L L I P Q A S S N 160  
 540 AATATACTTGAATGGAACATTCTTTCCATTCTAATAAAAGCTGGGATCTTCTTATCCACAGCAAGTTCAAAT  
 N N G N Y R C I G Y G D E N D V F R S N F I K I 186  
 617 AACAATGGCAATTATCGATGCATTGGATATGGAGATGAGAATGATGATTTAGATCAAATTTCAAATTAATAAAT  
 Q E L F P H P E L K A T D S Q P T E G N S V C 212  
 694 TCAAGAATATTTCCACATCCAGAGCTGAAAGCTACAGACTCTCAGCCTACAGAGGGGAATTCGTAAACCTGAGCT  
 E T Q L P P E R S D T P L H F N F R D G E V I L 237  
 771 GTGAAACACAGCTTCTCCAGAGCGGTGAGACACCCCACTTCACTTCACTTCTCAGAGATGGCGAGGTCATCTG  
 S D W S T Y P E L Q L P T V W R E N S G S Y W C G A 263  
 848 TCAGACTGGAGCAGTACCCGGAACCTCAGCTCCCAACCGTCTGGAGAGAAAACCTCAGGATCCTATTGGTGTGGTGC  
 E T V R G N I H K H S P S L Q I H V Q R I P V S G V 289  
 925 TGAAACAGTGAGGGGTAAATCCACAAGCACAGTCCCTCGCTACAGATCCATGTGCAGCGGATCCCTGTGTCTGGGG  
 L L E T Q P S G G Q A V E G E M L V L V C S V A E 314  
 1002 TGCTCCTGGAGACCCAGCCCTCAGGGGGCCAGGCTGTTGAAGGGGAGATGCTGGTCTTGTCTGCTCCGTGAGCTGAA  
 G T G D T T F S W H R E D M Q E S L G R K T Q R S L 340  
 1079 GGCACAGGGGATACCACATTCTCTGGCACCAGAGGACATGCAGGAGAGTCTGGGGAGGAAAACCTCAGCGTTCCCT  
 R A E L E L P A I R Q S H A G G Y Y C T A D N S Y G 366  
 1156 GAGAGCAGAGCTGGAGCTCCCTGCCATCAGACAGAGCCATGCAGGGGATACTACTGTACAGCAGACAACAGCTACG  
 P V Q S M V L V R E T P G N R D G L V A A G 391  
 1233 GCCCTGTCCAGAGCATGGTGAATGTCACTGTGAGAGAGACCCAGGCAACAGAGATGGCCTTGTGCGCCGCGGGA  
 A T G G L L S A L L L A V A L L F H C W R R R K S G 417  
 1310 GCCCTGGAGGGCTGCTCAGTGTCTTCTCCTGGCTGTGGCCCTGCTGTTCACTGCTGGCGTCGGAGGAAGTCAGG  
 V G F L G D E T R L P P A P G P G E S S H S I C P A 443  
 1387 AGTTGGTTTCTTGGGAGACGAAACCAGGCTCCCTCCCGCTCCAGGCCAGGAGATCCTCCCATTTCCATCTGCCCTG  
 Q V E L Q S L Y V D V H P K K G D L V Y S E I Q T 468  
 1464 CCCAGGTGGAGCTTCACTCGTTGTATGTATGTACACCCCAAAAGGAGATTGGTATCTCTGAGATCCAGACT  
 T Q L G E E E E A N T S R T L L E D K D V S V V Y S 494  
 1541 ACTCAGCTGGGAGAAGAAGAGGAAGCTAATACCTCCAGGACACTTCTAGAGGATAAGGATGTCTCAGTTGTCTACTC  
 E V K T Q H P D N S A G K I S S K D E E S \* 515  
 1618 TGAGGTAAGACACAACACCCAGATAACTCAGCTGGAAGATCAGCTCTAAGGATGAAGAAAGTTAAGAGAATGAAA  
 1695 AGTTACGGGAACGTCCTACTCATGTGATTTCTCCCTTGTCCAAGTCCCAGGCCAGTGCAGTCTTGCAGCACCTG  
 1772 GAATGATCAACTCATTCCAGCTTCTAATTCTTCTCATGATATGCATTCACTCCAGGAATACTCATTGCTCTACT  
 1849 CTGATGTTGGGATGGAATGGCCTCTGAAAGACTTCACTAAAATGACCAGGATCCACAGTTAAGAGAAGACCCTGTAG  
 1926 TATTTGCTGTGGGCTGACCTAATGCATTCCCTAGGGTCTGCTTTAGAGAAGGGGATAAAGAGAGAGAAGGACTGT  
 2003 TATGAAAAACAGAACACAAATTTGGTGAATTTGGGATTGTCAGAGATGAAAAAGACTGGGTGACCTGGATCTCTGC  
 2080 TTAATACATCTACAACCATTTGTCTCACTGGAGACTCACTTGCATCAGTTTGTTTAACTGTGAGTGGCTGCACAGGCA  
 2157 CTGTGCAAAACAATGAAAAGCCCTTCACTTCTGCCTGCACAGCTTACACTGTGAGGATTCAGTTGCAGATTAAAGAA  
 2234 CCCATCTGGAATGGTTTACAGAGAGAGGAATTTAAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC  
 2311 GCTTCCAAAAGCAAATGATAATTATGTTAATGTCAATTAGTGACAAAGATTGCAACATTAGAGAAAAGAGACACAAA  
 2388 TATAAAATTAATAAATAAGTACCAACTCTCCAAACTAAATTTGAACCTAAATATTAGTATAAACTCATAATAA  
 CTCTGCCTTTAAATAAAAAAAAAAAAAAAAAAAAAA

## IRTA1 cDNA and protein sequence

IRTA2A  
IRTA2C  
IRTA2B

1 RTA2B 1 CGGTGCAGTGTCTCTGACTGTGAAGATCAAGTCCAAACCTGTTTGGAAATTGAGGAAATCTCTCTTTTGATCTCAGCCCTTG  
 M L L W V I L L V L A P V S G Q F A R T P R 22  
 81 GTGGTCCAGGTCCTTCACTGCTGCTGGGTGATATTACTGGTCTGGCTCTGTCAGTGGACAGTTTGCAAGGACACCCAG  
 P I I F L Q P P W T T V F Q G E R V T L T C K G F R F 49  
 161 GCCCATTATTTTCCCTCCAGCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTACCCTCAGTCTGCAAGGGATTTCGCT  
 Y S P Q K K T K W Y H R Y L G K E I L R E T P D N I L 75  
 241 TCTACTCACCACAGAAAATAAAGTGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT  
 E V Q E S G E Y R C Q A Q G S P L S D L F S S 102  
 321 GAGGTTTCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTCTTCTT  
 A S L I L Q A P L S V F E G G D S V V L R C R A K A E A V 129  
 401 AGCTTCGCTGATCTCGAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGCAAGGCGGAAG  
 T L I Y K N D N V L A F L N K R T D F H I P H 155  
 481 TAACATGAATAATATCTATTACAAGAATGATATGCTGGCATTCTTAATAAAGAACTGACTTCCATATTTCTCAT  
 A C L K D N G A Y R C T G Y K E S C C P V S S N T V K 182  
 561 GCATGTCTCAAGGACAATGGTGCATATCGCTGTACTGGATATAAGGAAAGTTGTTGCCCTGTTTCTTCCAATACAGTCAA  
 I Q V Q E P F T R C P V L R A S S F Q P I S G N P V T L 209  
 641 AATCCTCAAGGACCTTACAGCTCCAGTCCAGTCCAGTCCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC  
 T C E T Q L S L E R S D V P L R F R F R D D Q T L 235  
 721 TGACCTGTGAGACCCAGTCTCTCTAGAGAGGTGAGATGTCCCGCTCCGGTTCGGTCTTTCAGAGATGACCAGACCCGTG  
 G L G W S L S P N F T Q C I A T M W S K D S G F Y W C K A 262  
 801 GGATTAGGCTGGAGTCTCTCCCGAATTCCAGATTACTGCCATTGGAGTAAGAAATTCAAGGTTCTACTGGTGAAGGC  
 A T M P H S V I S D S P R S W I Q V Q I P A S H P V L 289  
 881 AGCAACAATGCCTCACAGCGTCATATCTGACAGCCGAGATCTCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCTC  
 T L S P E K A L N F E G T K V T L H C E T Q E D S L 315  
 961 TCACTCTCAGCCCTGAAAGGCTCTGAATTTTGAGGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG  
 R T L Y R F Y H E G V P L R H K S V R C E R G A S I S 342  
 1041 CGCATTGTGACAGGTTTATCATGAGGGTGTCCTGAGGCACAAGTCAGTCCGCTGTGAAAGGGGAGCATCCATCAG  
 F S L T T E N S G N Y Y C T A D N G L G A K P S K A V 369  
 1121 CTCTCACTGACTACAGAGAATTCAGGGAACCTACTACTGCACAGTGACAATGGCCTTGGCGCAAGCCAGTAAGGCTG  
 S L S V T V P V S H P V L S P E D L I F E G A 395  
 1201 TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTCTCTGACCTCTCTCCTGAGGACCTGATTTTGAGGGAGCC  
 K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E 422  
 1281 AAGGTGACACTTCACTGTGAAGCCGAGAGGTTCACTCCCCATCTGTACCAGTTTCATCATGAGGATGTCGCCCTGGA  
 R R S A N S A G G V A I S F S L T A E H S G N Y Y C T 449  
 1361 GCGTAGGTGCGCAACTCTGCAGGAGGAGTGGCCATCAGCTTCTCTGACTGCAGAGCATTCAGGGAACCTACTACGCA  
 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475  
 1441 CAGCTGACAATGGCTTTGGCCCCAGCGCAGTAAGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCTGTCTC  
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502  
 1521 ACCCTCAGCTCTGTGAGGCCGCTGACTTTTGAAGGAGCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA  
 I L Y Q F Y H E D M P L T W S S S T P S V G R V S F S F 529  
 1601 AATCCTATACCAAGTTTATCATGAGGACATGCCCTGTGGAGCAGCTCAACACCTCTGTGGGAAGAGGTCTCTTCACT  
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555  
 1681 TCTCTCTGACTGAAGGACATTCAGGGAATTACTACTGCACAGCTGACAAATGGCTTTGGTCCCCAGCGCAGTGAAGTGGTG  
 S L F V T V P V S R P I L T L R V P R A Q A V V G D L 582  
 2A, 2C1761 AGCCTTTTGTCACTGTTCCTCAGTGTCTGCCCATCTCACCCTCAGGGTTCAGGGGCCAGGCTGTGGTGGGGGACCT  
 G K C W V L A S H P P L A E F S L T H S F K 582  
 2B 1761 -----GGTAAGTGTGGGTTCTTGCCAGTCAACCCATGGCTGTCTCTCACCATTCCCTTTAA  
 L E L H C E A P R G S P P I L Y W F Y H E D V T L G S 609  
 2A, 2C1841 GCTGGAGCTTCACTGTGAGGCCCGAGAGGCTCTCCCCAATCTGTACTGGTATTATCATGAGGATGTACCCCTGGGGA  
 N L F A L S S F L P \* stop 592  
 2B 1841 AAATCTGTTTGCAGTGTCCAGTTTCTCCCTAATCAACTTAATCCCCTTCTTGGCTTCTCTCAACTAACTAGCTGGG  
 S S A P S G G E A S F L T A E H S G C E 635  
 2A, 2C1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTTCACTCTCTGACTGCAGAACATTCTGGAACTACTCATGTGAG  
 2B 1921 GTTTTCCGTACTCATAAGTCTGGCTCAGCCAGACCCCTAAACAGCTCAGTAGATTCCCCAGCTTTTACCAATGAATT  
 A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662  
 2A, 2C2001 GCCAACATGGCCTAGTGGCCCCAGCACAGTACACAAATATCACTCAGTGTATAGTTCAGTATCTCGTCCCATCTCAC  
 2B 2001 TTTTATGTATTTCTCTCTCATTCTGTGATGTGCAACAGTACGCCAATTTTCTTGATGCACGGAGCGTGTCTACT  
 F R A P R A Q A V V G D L L E L H C E A L R G G S S P I 689  
 2A, 2C2081 CTTACAGGCTCCCAGGGGCCAGGCTGTGGTGGGGGACTGCTGAGCTTCACTGTGAGGCCCTGAGAGGCTCTCTCCCA  
 2B 2081 TCTCTACTGACATTTACATATTAACCTAGCTACAAGCACAGTCTTATAGATAAATATGGTCAAGACCTTAAATCTCCCA

[illegible]

FIGURE 18B-3

4081 ATGCTGATGCTGCTGGCCCTGGGACTGCACTGCATGCATGTGAAGCCCTATAGGTCTCAGCAGAGGCCCATGGAGAGGGA  
4161 ATGTGTGGCTCTGGCTGCCAGGGCCCAACTCGGTTTACACGGATCGTGCTGCTCCCTGGCCAGCCTTTGGCCACAGCAC  
4241 CACCAGCTGCTGTTGCTGAGAGAGCTTCTTCTGTGACATGTTGGCTTTCATCAGCCACCTGGGAAGCGGAAAGTAGC  
4321 TGCCACTATCTTTGTTTCCCACTCAGGCCTCACACTTCCCATGAAAAGGTGAATGTATATAACCTGAGCCCTCTCC  
4401 ATTCAGAGTTGTTCTCCCATCTCTGAGCAATGGGATGTTCTGTTCCGCTTTTATGATATCCATCACATCTTATCTTGATC  
4481 TTTGCTCCAGTGGATTGTACAGTGATGACTTTAAGCCCCACGGCCCTGAAATAAAATCCTTCCAAGGGCATTGGAAGC  
4561 TCACTCCACCTGAACCATGGCTTTTGTATGCTTCCAAGTGTGAGGCTGTATGCAGCCAGTGCAGCCTTGACAGGCAAGGCTG  
4641 CAACCTTTCAAGGAGGAAACCAGACACCTGAGACAGGAGCTGTATGCAGCCAGTGCAGCCTTGACAGGCAAGGCTG  
4721 GAGGCATTTGTCTCATCACTACAGATATGCAACTAAAATAGACGTGGAGCAAGAGAAATGCATTCEGACCGAGGCCGCTTTT  
4801 TTAGGCCCTAGTTGAAAGTCAAGAAGGACAGCAGCAAGCATAGGCTCAGGATTAAAGAAAAAATCTGCTCACAGTCTGTT  
4881 CTGGAGGTCACATCACCACAAAGCTCACGCCCTATGCAGTTCTGAGAAGGTGGAGGCACAGGCTCAAAAGAGGAAAT  
4961 TAGAATTTCTCATTGGGAGAGTAAGGTACCCCATCCAGAAATGATAACTGCACAGTGGCAGAACAACTCCACCTAAT  
5041 GTGGGTGGACCCCATCCAGTCTGTTGAAGGCCCTGAATGTAACAAAGGGCTTATTCTTCTCAAGTAAGGGGAACTCCT  
5121 GCTTTGGGCTGGGACATAAGTTTCTGCTTTCAGACGCAAACTGAAAAATGGCTCTTCTTGGGTCTTGAGCTTGCTGGC  
5201 ATATGGACTGAAAGAACTATGCTATTGGATCTCCTGGATCTCAGCTTGCTGACTGCAGATCTTGAGATATGTCAGCCT  
5281 CTACAGTCACAAGAGCTAATTCATCTAATAAACCAATCTTC

## FIGURE 18C-1

1 AGTGAAGGGGTTTCCCATATGAAAAATACAGAAAGAATTATTTGAATACTA  
52 GCAAATACACAACCTTGATATTTCTAGAGAACCAGGCACAGTCTTGGAGAC  
103 ATTACTCCTGAGAGACTGCAGCTGATGGAAGATGAGCCCCAAGTCTTAAAA  
154 ATGTATCACTACCGGGATTGAGATACAAACAGCATTTAGGAAGGTCTCATC  
205 TGAGTAGCAGCTTCTGCCCCTCCTTCTTGGAGATAAGTCGGGCTTTTGGTG  
256 AGACAGACTTTCCCAACCTCTGCCCGCCGGTGCCCATGCTTCTGTGGCT  
1 M L L W L  
307 GCTGCTGCTGATCCTGACTCCTGGAAGAGAACAATCAGGGGTGGCCCCAAA  
6 L L L I L T P G R E Q S G V A P K  
358 AGCTGTACTTCTCCTCAATCCTCCATGGTCCACAGCCTTCAAAGGAGAAAA  
23 A V L L L N P P W S T A F K G E K  
409 AGTGGCTCTCATATGCAGCAGCATATCACATTCCCTAGCCCAGGAGACAC  
40 V A L I C S S I S H S L A Q G D T  
460 ATATTGGTATCAGATGAGAAGTTGTTGAAAAATAACATGACAAGATCCA  
57 Y W Y H D E K L L K I K H D K I Q  
511 AATTACAGAGCCTGGAAATTACCAATGTAAGACCCGAGGATCCTCCCTCAG  
74 I T E P G N Y Q C K T R G S S L S  
562 TGATGCCGTGCATGTGGAATTTTCACTGACTGGCTGATCCTGCAGGCTTT  
91 D A V H V E F S P D W L I L Q A L  
613 ACATCCTGTCTTTGAAGGAGACAATGTCTTCTGAGATGTGAGGGGAAAGA  
108 H P V F E G D N V I L R C Q G K D  
664 CAACAAAAACACTCATCAAAGGTTTACTACAAGGATGAAAAACAGCTTCC  
125 N K N T H Q K V Y Y K D G K Q L P  
715 TAATAGTTATAATTTAGAGAAGATCACAGTGAATTCAGTCTCCAGGGATAA  
142 N S Y N L E K I T V N S V S R D N  
766 TAGCAAAATATCATTGTACTGCTTATAGGAAGTTTACATACTTGACATTGA  
159 S K Y H C T A Y R K F Y I L D I E  
817 AGTAACTTCAAAACCCCTAAATATCCAAGTTCAAGAGCTGTTTCTACATCC  
176 V T S K P L N I Q V Q E L F L H P  
868 TGTGCTGAGAGCCAGCTCTTCCACGCCCATAGAGGGGAGTCCCATGACCCT  
193 V L R A S S S T P I E G S P M T L  
919 GACCTGTGAGACCCAGCTCTCTCCACAGAGGCCAGATGTCCAGCTGCAATT  
210 T C E T Q L S P Q R P D V Q L Q F  
970 CTCCTCTTCAAGATAGCCAGACCCTCGGATTGGGCTGGAGCAGGTCCCC  
227 S L F R D S Q T L G L G W S R S P  
1021 CAGATCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCTTACTGGTG  
244 R L Q I P A M W T E D S G S Y W C  
1072 TGAGGTGGAGACAGTGACTCACAGCATCAAAAAAGGAGCCTGAGATCTCA  
261 E V E T V T H S I K K R S L R S Q  
1123 GATACGTGTACAGAGAGTCCCTGTGTCTAATGTGAATCTAGAGATCCGGCC  
278 I R V Q R V P V S N V N L E I R P  
1174 CACCGGAGGCGAGTGATTGAAGGAGAAAAATATGGTCCTTATTGCTCAGT  
295 T G G Q L I E G E N M V L I C S V  
1225 AGCCCAGGGTTTCAAGGACTGTACATTCTCCTGGCACAAGAAGGAGAGT  
312 A Q G S G T V T F S W H K E G R V  
1276 AAGAAGCCTGGGTAGAAAGACCCAGCGTTCCCTGTTGGCAGAGCTAGTG  
329 R S L G R K T Q R S L L A E L H V  
1327 TCTCACCGTGAAGGAGAGTGATGCAGGGAGATACTACTGTGCAGCTGATAA  
346 L T V K E S D A G R Y Y C A A D N  
1378 CGTTCACAGCCCCATCCTCAGCACGTGGATTTCAGTACCCGTGAGAATTCC  
363 V H S P I L S T W I R V T V R I P  
1429 GGTATCTCACCTGTCTCACCTTCAGGGCTCCCGGGCCCACTGTGGT  
380 V S H P V L T F R A P R A H T V V  
1480 GGGGACCTGCTGGAGCTTCACTGTGAGTCCCTGAGAGGCTCTCCCCGAT  
397 G D L L E L H C E S L R G S P P I  
1531 CCTGTACCGATTATCATGAGGATGTACCCCTGGGGAACAGCTCAGCCCC  
414 L Y R F Y H E D V T L G N S S A P  
1582 CTCTGGAGGAGGAGCCTCCTTCAACCTCTCTGACTGCAGAATCTCTGG  
431 S G G G A S F N L S L T A E H S G  
1633 AAATACTCCTGTGATGCAGACAATGGCCTGGGGGCCAGCACAGTCATGG  
448 N Y S C D A D N G L G A Q H S H G  
1684 AGTGAGTCTCAGGGTCACAGTTCGGGTGTCTCGCCCCGTCTCACCTCAG  
465 V S L R V T V P V S R P V L T L R  
1735 GGCTCCCGGGGCCAGGCTGTGGTGGGGGACCTGCTGGAGCTTCACTGTGA  
483 A P G A Q A V V G D L L E L H C E  
1786 GTCCCTGAGAGGCTCCTTCCCGATCCTGTACTGGTTTATCACGAGATGA  
499 S L R G S F P I L Y W F Y H E D D  
1837 CACCTTGGGGAAATCTCGGCCCACTCTGGAGGAGGGGCATCCTTCAACCT  
516 T L G N I S A H S G G G A S F N L  
1888 CTCTCTGACTACAGAATCTTGGAACTACTCATGTGAGGCTGACAAATGG  
533 S L T T E H S G N Y S C E A D N G

1939 CCTGGGGGCCAGCAGCAGTAAGGTGGTGCACACTCAATGTTACAGGAACCTC  
550 L G A Q H S K V V T L N V T G T S  
1990 CAGGAACAGAACAGGCCTTACCGCTGCGGGAATCAGGGGCTGGTGTCTCAG  
567 R N R T G L T A A G I T G L V L S  
2041 CATCCTCGTCCTTGTCTGCTGCTGCTCTGCTGCATTACGCCAGGCCCCG  
584 I L V L A A A A A L L H Y A R A R  
2092 AAGGAACAGGAGGACTTCTGCCATCGGAACATCTAGTCACAGTCCTAG  
601 R K P G G L S A C T G T S H S P S  
2143 TGAGTGTCTAGGAGCCTTCTCTCGTCCAGGCCTTCCAGGATAGCCCTCAAGA  
618 E C Q E P S S S R P S R I D P Q E  
2194 GCCCATCTACTCTAAACCATAGCCCCAATGGAGCTGGAGCCATGTACAG  
635 P T H S K P L A P M E L E P M Y S  
2245 CAATGTAAATCTGGAGATAGCAAGCGATTATTTCCAGATCTGGAGCAT  
652 N V N P G D S N P I Y S Q I W S I  
2296 CCAGCATACAAAAGAAAACAGCTAATTGTCCATGATGCATCAAGAGCA  
669 Q H T K E N S A N C P M M H Q E H  
2347 TGAGGAACCTTACAGTCTCTATTTCAGAACTGAAGAAGCACACCCAGACGA  
686 E E L T V L Y S E L K K T H P D D  
2398 CTCTGCAGGGGAGGCTAGCAGCAGAGGCAGGCCCCATGAAGAAGATGTGA  
703 S A A G E A S S R G R A H E E D D E  
2449 AGAAACTATGAGAATGTACCAGTGTATTACTGGCTCAGACCCACTAGCC  
720 E N Y E N V P R V L L A S D H  
2500 CCTTACCCAGAGTGGCCCCACAGGAACAGCCTGCACCATTTTTTTTCTGT  
2551 TCTCTCCAAACACATCATCCATCTCTCCAGACTCTGCCTCTACGAGGC  
2602 TGGGCTGCAGGGTATGTGAGGCTGAGCAAAGGCTCGCAATCTCCCTGT  
2653 GCCTGATCTGTGTGTTCCCCAGGAAGAGAGCAGGCAGCCTCGAGCAAGCA  
2704 CTGTGTTATTTTCACAGTGGAGACAGTGGCAAGGCAGGAGGGCCCTCAGC  
2755 TCCTAGGGCTTCGAATAGAGGAGGAGAGAGAAATGGTCTAGCGGGTTA  
2805 CAAGGGCACAATCATGACCAATTTGATCCAACTGTGATCGAAAGCTGTTAAT  
2857 GTGCTCTCTGTATAACAATTTGCTCCAAATATTTGTGTTTCCCTTTTGT  
2908 GTGGCTGGTAGTGGCATTTGCTGATGTTTTGGTGTATATGCTGTATCCTTGC  
2959 TACCATTATTTGGG

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FIGURE 18D-1

1 TGGTGACCAAGAGTACATCTCTTTTCAAATAGCTGGATTAGGTCCTCATGC  
19 L W S L L V I F D A V T E Q A D S  
103 CGCTGACCCTTGTGGCGCCCTCTTCTGTCTTGAAGGAGACAGCATCGTTC  
36 L T L V A P S S V F E G D S I V L  
154 TGAATGCCAGGGAGAACAGAACTGGAAAATTGAGAAGATGGCTTACCATA  
53 K C Q G E Q N W K I Q K M A Y H K  
205 AGGATAACAAGAGTTATCTGTTTCAAAAAATTCTCAGATTCTCTTATCC  
70 D N K E L S V F K K F S D F L I Q  
256 AAAGTGCAGTTTAAAGTGACAGTGGTAATTTCTGTAGTACCAAGGAC  
87 S A V L S D S G N Y F C S T K G Q  
307 AACTCTTCTCTGGGATAAACTTCAAATATAGTAAAGATAAAAGTCCAAG  
104 L F L W D K T S N I V K I K V Q E  
358 AGCTCTTCAACGTCCTGTGCTGACTGCCAGCTCTTCCAGCCCATCGAAG  
121 L F Q R P V L T A S S F Q P I E G  
409 GGGTCCAGTGAGCCTGAAATGTGAGACCCGGCTCTTCCACAGAGGTGG  
138 G P V S L K C E T R L S P Q R L D  
460 ATGTTCAACTCCAGTTCTGCTTCTTCAGAGAAAACAGGTCCTGGGGTCAG  
155 V Q L Q F C F F R E N Q V L G S G  
511 GCTGGAGCAGCTCTCCGGAGCTCCAGATTTCTGCCGTGTGGAGTGAAGACA  
172 W S S S P E L Q I S A V W S E D T  
562 CAGGGTCTTACTGGTGCAAGGCAGAAACGGTGACTCACAGGATCAGAAAAC  
189 G S Y W C K A E T V T H R I R K Q  
613 AGAGCCTCAATCCAGATTACGTGCAGAGAATCCCCATCTCTAATGTAA  
206 S L Q S Q I H V Q R I P I S N V S  
664 GCTTGAGATCCGGGCCCCGGGGGACAGGTGACTGAAGGACAAAACTGA  
223 L E I R A P G G Q V T E G Q K L I  
715 TCCTGCTCTGCTCAGTGGCTGGGGTACAGGAAATGTACATTCTCCTGGT  
240 L L C S V A G G T G N V T F S W Y  
766 ACAGAGAGGCCACAGGAACAGTATGGGAAAGAAAACCCAGCGTCCCTGT  
257 R E A T G T S M G K K T Q R S L S  
817 CAGCAGAGCTGGAGATCCAGCTGTGAAAGAGAGTGATGCCGGCAAAATTT  
274 A E L E I P A V K E S D A G K Y Y  
868 ACTGTAGAGCTGACAACGGCCATGTGCCTATCCAGAGCAAGGTGGTGAATA  
291 C R A D N G H V P I Q S K V V N I  
919 TCCCTGTGAGAAATCCAGTGTCTCGCCCTGTCTCACCTCAGGTCTCCTG  
308 P V R I P V S R P V L T L R S P G  
970 GGGCCCCAGGCTGCAGTGGGGACCTGTGGAGCTTCACTGTGAGGCTCACCTTG  
325 A Q A A V G D L L E L H C E A L R  
1021 GAGGCTCTCCCCAATCTGTACCAATTTATCATGAGGATGTACCCCTTG  
342 G S P P I L Y Q F Y H E D V T L G  
1072 GGAACAGCTCGGCCCCCTCTGGAGGAGGGCCTCCTTCAACTCTCTTTGA  
359 N S S A P S G G G A S F N L S L T  
1123 CTGCAGAACATTCTGGAATACTCCTGTGAGGCCAACACCGCCTGGGG  
376 A E H S G N Y S C E A N N G L G A  
1174 CCCAGTGCAGTGAGGAGTCCAGTCTCCATCTCAGGACCTGATGGCTATA  
393 Q C S E A V P V S I S G P D G Y R  
1225 GAAGAGACCTCATGACAGCTGGAGTTCTCTGGGGACTGTTGGTGTCTTG  
410 R D L M T A G V L W G L F G V L G  
1276 GTTCACTGGTGTGCTTTGCTGTGTATGCCTTGTCCACAAGATATCAG  
427 F T G V A L L L Y A L F H K I S G  
1327 GAGAAAGTTCTGCCACTAATGAACCCAGAGGGCTTCCAGGCCAAATCCTC  
444 E S S A T N E P R G A S R P N P Q  
1378 AAGAGTTACCTATTCAAGCCCAACCCAGACATGGAGGAGCTGCAGCCAG  
461 E F T Y S S P T P D M E E L Q P V  
1429 TGTATGCAATGTGGGCTCTGTAGATGTGGATGTGGTTTATTCTCAGTCT  
478 Y V N V G S V D V D V V Y S Q V W  
1480 GGAGCATGCAGCAGCCAGAAAGCTCAGCAACATCAGGACACTTCTGGAGA  
495 S M Q Q P E S S A N I R T L L E N  
1531 ACAAGGACTCCCAAGTCATCTACTTCTGTGAAGAAATCATAACACTTG  
512 K D S Q V I Y S S V K K S  
1582 AGGAATCAGAAGGAAGATCAACAGCAAGGATGGGGCATTAAGACTTG  
1633 CTATAAAACCTTATGAAATGCTTGAGGCTTATCACTGCCACAGCCAGAA  
1684 CTGCTCAGGAGGCACCTCCTGTCTTTTGTCTGATGATGTTCTTCT  
1735 CCAATATCTCTTTTACCTATCAATATTCTTGAAGCAATCAGTGTG  
1786 AACTGTGCAAAATAAATTTCTGCTACCTTCTCTTAAGCAATCAGTGTG  
1837 TAAAGATTTGAGGGAAGAATGAATAAGAGATACAAGGTCTCACCTTCTAT  
1888 ACTGTGAAGTATGAGAACAGGACTTGATAGTGGTGTATTAACTTATTAT  
1939 GTGCTGCTGGATACAGTTTGCTAATATTTTGTGAGAATTTTGTCAAATAT

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FIGURE 18D-2

1990 GTTCATTGGGAATATTGGCCTGAAATTTCTTTTCCACTGTGTCTCTGCCA  
2041 GAATGTTTGTATCAGGCTGATGCTGGCTTCATAGAATGAGTTAGGCAGGAG  
2092 CCCTTCCTCCTTGATTTTGGCATAGTTTCAGCAGGATTGGTACCAGTTA  
2143 TTCTTTCTGCATCTGTAGAATTCAGCTATGAATCCATCTGGTCTAGGGCT  
2194 TTTGTGTGGTTGGTAAGTTTTTATTACTAATCAACTTCAGCGCTTGAT  
2245 ATTGGTCTAGGAGGGGTTCTGTCTCTTCTGGTTCAATCTTGGGAGATTG  
2296 TGTGTTCCAGGAATTTAGCCGTTTCTCCAGATTTCTTCTTTATGTGCA  
2347 TCGACTTGAGTGTAACATAACTTATATGCACTGGGAAACCAAAAATCTG  
2398 TGTGACTTGCTTTATTGCAAGTATGCATATAGTTGCAAAAATGTGATTTTGA  
2449 ACCTGCAATATCACCAAAGTATGCATATAGTTGCAAAAATGTGATTTTGA  
2500 CATAGTAAATATGAGTATTTGCAATAAATATGATATTACTTTTGAAGTA  
2551 TATAGAATAAAATGTAATAATCTATAAAA



FIGURE 18E-1

1 GAGGCATCTCTAGGTACCATCCCTGACCTGGTCCTC  
 37 ATGCTGCCGAGGCTGTTGCTGTTGATCTGTGCTCCACTCTGTGAA  
 M L P R L L L L I C A P L C E 15  
 82 CCTGCCGAGCTGTTTTGATAGCCAGCCCTCCCATCCACAGAG  
 P A E L F L I A S P S H P T E 30  
 127 GGGAGCCAGTGACCTGACGTGTAAGATGCCCTTTCTACAGAGT  
 G S P V T L T C K M P F L Q S 45  
 172 TCAGATGCCAGTTCCAGTTCTGCTTTTTCAGAGACACCCGGGCC  
 S D A Q F Q F C F F R D T R A 60  
 217 TTGGGCCAGGCTGGAGCAGCTCCCCAAGCTCCAGATCGCTGCC  
 L G P G W S S S P K L Q I A A 75  
 262 ATGTGGAAGAAGACACAGGGTCATACTGGTGGCAGGCACAGACA  
 M W K E D T G S Y W C E A Q T 90  
 307 ATGGCGTCCAAAGTCTTGAGGAGCAGGAGATCCAGATAAATGTG  
 M A S K V L R S R R S Q I N V 105  
 352 CACAGGGTCCCTGTGCTGATGTGAGCTTGGAGACTCAGCCCCCA  
 H R V P V A D V S L E T Q P P  
 397 GGAGGACAGGTGATGGAGGGAGACAGGCTGGTCTCATCTGCTCA  
 G G Q V M E G D R L V L I C S  
 442 GTTGCTATGGGCACAGGAGACATCACCTTCTTTGGTACAAAGGG  
 V A M G T G D I T F L W Y K G  
 487 GCTGTAGGTTTAAACCTTCAGTCAAAGACCCAGCGTTCAGTGACA  
 A V G L N L Q S K T Q R S L T  
 532 GCAGAGTATGAGATTCTTCAGTGAGGAGAGTGATGCTGAGCAA  
 A E Y E I P S V R E S D A E Q  
 577 TATTACTGTGTAGCTGAAAATGGCTATGGTCCCAGCCCCAGTGGG  
 Y Y C V A E N G Y G P S P S G  
 622 CTGGTGAGCATCACTGTGAGAATCCCGGTGTCTCGCCCAATCCTC  
 L V S I T V R I P V S R P I L 210  
 667 ATGCTCAGGGCTCCCAGGGCCAGGCTGCAGTGGAGGATGTGCTG  
 M L R A P R A Q A A V E D V L  
 712 GAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCTCCAATCCTGTAC  
 E L H C E A L R G S P P I L Y  
 757 TGGTTTTATCACGAGGATATCACCTGGGGAGCAGGTGCGCCCCC  
 W F Y H E D I T L G S R S A P  
 802 TCTGGAGGAGGAGCCTCCTCAACCTTCCCTGACTGAAGAACAT  
 S G G G A S F N L S L T E E H  
 847 TCTGGAAACTACTCCTGTGAGGCCAACAATGGCCTGGGGGCCAG  
 S G N Y S C E A N N G L G A Q  
 892 CGCAGTGAGGCGGTGACACTCAACTTCACAGTGCCCTACTGGGGCC  
 R S E A V T L N F T V P T G A  
 937 AGAAGCAATCATCTTACCTCAGGAGTCATTGAGGGGCTGCTCAGC  
 R S N H L T S G V I E G L L S 315  
 982 ACCCTTGGTCCAGCCACCGTGGCCTTATTTTGTCTACGGCCTC  
 T L G P A T V A L L F C Y G L  
 1027 AAAAGAAAAATAGGAAGACGTTTACGCCAGGGATCCACTCAGGAGC  
 K R K I G R R S A R D P L R S  
 1072 CTTCGCCAGCCCTTACCCCAAGAGTTACCTACCTCAACTCACCT  
 L P S P L P Q E F T Y L N S P  
 1117 ACCCCAGGGCAGCTACAGCCTATATATGAAAATGTGAATGTTGTA  
 T P G Q L Q P I Y E N V N V V  
 1162 AGTGGGGATGAGGTTTATTCACTGGCGTACTATAACCAGCCGGAG  
 S G D E V Y S L A Y Y N Q P E  
 1207 CAGGAATCAGTAGCAGCAGAAACCCCTGGGGACACATATGGAGGAC  
 Q E S V A A E T L G T H M E D  
 1252 AAGGTTTCCTTAGACATCTATTCCAGGCTGAGGAAAGCAAACATT  
 K V S L D I Y S R L R K A N I 330  
 1297-ACAGATGTGGACTATGAAGATGCTATGTAA 1326 339  
 T D V D Y E D A M \*  
 GGT ATGGAAGATT CTGCTCTTTG  
 1351 AAAACCATCC ATGACCCCAA GCCTCAGGCC TGATATGTTT TTCAGAGATC  
 1401 CTGGGGCATT AGCTTTCCAG TATACCTCTT CTGGATGCCA TTCTCCATGG  
 1451 CACTATTCTT TCATCTACTG TGAAGTGAAG TTGGCGCAGC CCTGAAGAAA  
 1501 CTACCTAGGA GAACATAAG ACACAGGAGT GACAGGGACT TTGTTATCAG  
 1551 AACCAGATTCT CTGCCGGCTC CTTTGAAGAAC AGGTCAATAT GTGCTCTTCT  
 1601 GTTTACAAGA GGAAACAAGA TGAATAAAA GAAATTGGGA TCCTGGGTTG  
 1651 GAGGGACAGT GAAGCTTAGA GCACATGAAC TCAAGGTTAG TGACTCTGCA  
 1701 GGACTTCACA GAGAGAGCTG TGCCCATCAT TCAGTCCAAG TGCTTTCTCT  
 1751 GCCCAGACAG CACAGAACTC CAGCCCCGCT ACTTACATGG ATCATCGAGT  
 1801 TTCCACCTAA AATATGATTC TATTTATTTT GAGTCACTGT TACCAAATTA

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[illegible]